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Sequence

2, Appli 38, Appl 11, Appl 11, Appl 11, Appl 11, Appl 12, Appli 2, Appli 3, Appli 3, Appli 3, Appli 4, Appli 5, Appli 6, Appli 7, Appli 7, Appli 7, Appli 8, Appli 9, Appli 9,

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Maximum DB
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Perfect score:
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Match
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1: /ggn2_6/ptodata/1/iaa/5_COMB.pep:*

2: /cgn2_6/ptodata/1/iaa/6_COMB.pep:*

3: /ggn2_6/ptodata/1/iaa/H_COMB.pep:*

4: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

5: /ggn2_6/ptodata/1/iaa/RE_COMB.pep:*

6: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
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US-08-463-01818-26
US-08-463-0748-26
US-08-465-585C-26
US-08-652-446-26
US-08-652-446-26
US-09-237-543-7
US-09-644-450-8
US-09-237-543-2
US-09-237-543-2
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Biocceleration Ltd
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Patent No. 6143540
GENERAL INFORMATION:
APPLICANT: KADELIEY, ROSANA
TITLE OF INVENTION: NOVEL MOLECULES OF THE HK
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: 035800/175631
CURRENT APPLICATION NUMBER: US/09/237,543A
CURRENT FILING DATE: 1999-01-26
NUMBER OF SEQ ID NOS: 11
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO
LENGTH: 313
TYPE: PAT
ORGANISM: Homo sapiens
US-09-237-543-9
 RESULT 2
US-09-644-450-9
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Matches 313
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US-10-803-277-2
US-10-803-277-2
US-10-355-975A-38
US-09-579-664B-11
US-09-570-170-6
US-09-964-956-72
US-09-770-170-2
US-09-170-170-2
US-09-181-2
US-09-181-2
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US-09-181-2
US-10-283-247-2
US-10-283-247-7
US-10-283-247-7
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US-10-283-247-7
US-08-817-832B-3
US-08-817-832B-3
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Pred. No. 7.5e-161;
Mismatches 0;
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Indels Length

0;

Gaps

300 240 240 180 180 120 120 60 60 Search. History

Result

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FRICEIC NO. 1007.

FRIEDRIA INFORMATION:
APPLICANT: Kapeller, Rosana
TITLE OF INVENTION: NOVEL MOLECULES OF THE HK1
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: 035800/175631
CURRENT APPLICATION NUMBER: US/09/644,450
CURRENT FILING DATE: 2000-08-23
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 9
LENGTH: 313
TYPE: PRT
ORGANISM: Homo sapiens
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Patent No. 6383791
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Best Local Similarity
Matches 313; Conserv
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                                                                                                                                                                                                                                                                                                                                              Patent No. 5871960 5837487
                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC comparible
COMPUTER: TEM PC COMPATION
SOFTMARE: Version #1.0,
SOFTMARE: Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                APPLICANT: Smith, Kendall A. & Beadling, Carol
TITLE OF INVENTION: Nucleic Acids Encoding CR5 Polypeptide,
TITLE OF INVENTION: Vector and Transformed Cell Thereof, and Expression Thereof
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: PRETTY, SCHROEDER & POPLAWSKI
STREET: 444 South Flower St. - Suite 1900
PRIOR APPLICATION DATA:
                                                                                                                                                      STREET: 444 South |
CITY: LOS Angeles
STATE: California
COUNTRY: USA
ZIP: 90071
             APPLICATION NUMBER: US/
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                            US/08/463,081B
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TOPOLOGY: n.a.
; MOLECULE TYPE: peptide
US-08-463-081B-26
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Best Local Similarity 99.4%;
Matches 311; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 08/104,736
FILING DATE: 10-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/796,066
FILING DATE: 20-NOV-91
ATTORNEY/AGRET INFORMATION:
NAME: Viviana Amzel, Ph. D.
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: 966 38150 (DART-060)
TELECHONE: (213) 622-7700
TELECHONE: (213) 622-7700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (213) 622-7700
TELEPAX: (213) 489-4210
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 313 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
STRANDEDNESS: n.a.
301
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  EIHLHSLSPGPSK 313
                           EIHLHSLSPGPSK 313
                                                                                                                 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA
                                                                                                                                                                        ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI
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US-08-461379A-26

VS-08-461379A-26

VS-08-461379A

Patent No. 5871961

GENERAL INFORMATION:

APPLICANT: Smith, Kendall A. & Beadling, Carol

APPLICANT: Smith, Kendall A. & Beadling, Carol

TITLE OF INVENTION: Nucleic Acids Encoding CR5 Polypeptide,

TITLE OF INVENTION: Vector and Transformed Cell Thereof, and

TITLE OF INVENTION: Expression Thereof

NUMBER OF SEQUENCES: 35

CORRESPONDENCE ADDRESS:

ADDRESSEE: (B) STREET:One Westlakes-Berwyn

CITY: Valley Forge

STATE: Pennsylvania

COUNTRY: USA

IP: 19482

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Version #1.25

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FILING DATE: 5-UNE-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/330,108; 08/104,736
APPLICATION NUMBER: USSN 08/330,108; 08/104,736
APPLICATION NUMBER: & 07/796,066
FILING DATE: 27-CCT-1994; 10-AUG-1993 & 20-NOV-91
ATTORNEY/AGENT INFORMATION:
NAME: Viviana Anzel, Ph. D.
REGISTRATION NUMBER: DART-070
REFERENCE/DOCKET NUMBER: DART-070
TELECOMMUNICATION INFORMATION:
TELEPAN: (610)470-0700
TELEPAN: (610)470-0700
TELEPAN: (610)470-0701
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LERGIST. 313 anio 20 466
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US-08-462-390B-26
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COUMINI.
ZIP: 19482
COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPETWARE: Patentin Release #1.0, Ve
                                                                                                                                                                                                                         Sequence 26, Application US/08462390B
Patent No. 5882894
GENERAL INFORMATION:
APPLICANT: Smith, K. A., & Beadling, C.
TITLE OF INVENTION: Nucleic Acids Encoding CR8 Polypeptide, Vector and TITLE OF INVENTION: Transformed Cell Thereof, and Expression Thereof NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ratner & Prestia
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STRANDEDNESS: n.a.
TOPOLOGY: n.a.
MOLECULE TYPE: peptide
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                                                                                                                                                     STATE: E
                                                                                                                                                                                       CITY: Valley Forge
                                                                                                                                                                                                             ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
les 311; Conserv
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Pred. No. 1.6e-159;
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                                      Version
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                                                                                                                                       Sequence 26, Application US/08463074B
Patent No. 6020155
GENERAL INFORMATION:
APPLICANT: Smith, Kendall A. & Beadling, Carol
TITLE OF INVENTION: Nucleic Acids Encoding CR1
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 311; Conservative
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Best Local Similarity
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INFORMATION FOR SEQ ID NO:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Viviana Amzel, Ph. D.
REGISTION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: DAI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (610)407-0700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/462,390B
FILING DATE: 5-JUNE-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/330,108
FILING DATE: 27-0CT-1994
FILING DATE: 27-0CT-1994
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ATTORNEY/AGENT INFORMATION:
                                                                             CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: peptide STRANDEDNESS: n.a.
                                                             COUNTRY: USA
                                                                                                          ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: USSN 08/104,736
FILING DATE: 10-AUG-1993
APPLICATION NUMBER: USSN 07/796,066
                                                                                                                           ADDRESSEE:
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(610)407-0701
OR SEQ ID NO: 26:
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                                                                                                                           SCHROEDER & POPLAWSKI
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                                                                                                          Flower St.
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FILING DATE: 5-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/104,736
FILING DATE: 10-AUG-1993
PRIOR APPLICATION NUMBER: US 07/796,066
FILING DATE: 20-NOV-91
APPLICATION NUMBER: US 07/796,066
FILING DATE: 20-NOV-91
ATTORNEY/AGENT INFORMATION:
NAME: VY1ana AMZE1, Ph. D.
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: P66 38143 (DART-020)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-4210
INFORMATION FOR SEQ ID NO: 26:
CECOIPENCE (213) 489-4210
INFORMATION FOR SEQ ID NO: 26:
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                                                                                                                                                                                                                 Sequence 26, Application US/08465585C Patent No. 6027914 GENERAL INFORMATION:
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Best Local Similarity
                                                                                                               APPLICANT: Smith, K. A., & Beadling, C.
TITLE OF INVENTION: Nucleic Acids Encoding CR6 Polypeptide, Vecto
TITLE OF INVENTION: Transformed Cell Thereof, and Expression Thereof
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
SOFTWARE: Version #1.25
CURRENT APPLICATION DATA:
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LENGTH: 313 amino acids
CITY: Los Angeles
STATE: Californiaa
COUNTRY: USA
ZIP: 900071
                                                                        ADDRESSEE:
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                                                                                                PRETTY, SCHROEDER & POPLAWSKI
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                                                                                  STREET
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Pred. No. 1.6e-159;
0; Mismatches 2;
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                                                                          Sequence 26, Application US/08652446
Patent No. 6657427
GENERAL INFORMATION:
APPLICANT: Smith, Kendall A. & Beadling, Carol
APPLICANT: Mucleic Acids Encoding CR5
TITLE OF INVENTION: Nucleic Acids encoding CR5
TITLE OF INVENTION: Polypeptide, Vector and Transformed Cell Thereof,
TITLE OF INVENTION: Expression Thereof
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NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: PRETTY, S

ADDRESSEE:

PRETTY, SCHROEDER & POPLAWSKI
. (B) STREET:

444

South Flower St.

Suite 1900

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US-08-652-446-26
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                    RESULT 8
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Best Local Similarity
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INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/465,585C FILING DATE: 5-JUNE-1995 PRIOR APPLICATION DATA: APPLICATION NUMBER: USSN 08/330,108 FILING DATE: 27-OCT-1994 APPLICATION NUMBER: USSN 08/104,736 FILING DATE: 10-AUG-1993 APPLICATION NUMBER: USSN 07/796,066 FILING DATE: 10-AUG-1993 APPLICATION NUMBER: USSN 07/796,066 FILING DATE: 10-AUG-1993 APPLICATION NUMBER: USSN 07/796,066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Viviana Amzel, Ph. D.
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: P66
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 622-7700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: n.a. MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 20-NOV-1991
ATTORNEY/AGENT INFORMATION:
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                                                                                                    EIHLHSLSPGPSK 313
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                                                                              EIHLHSLSPGPSK 313
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Pred. No. 1.6e-159;
0; Mismatches 2;
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FILING DATE: 5-JUN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/330,108
FILING DATE: 27-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/463,074
FILING DATE: 5-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/462,337
FILING DATE: 5-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
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APPLICATION DATA:
APPLICATION DATA:
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PRIOR APPLICATION UNWEER: 08/465,585
PRIOR APPLICATION UNWEER: 08/465,585
FILING DATE: 5-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION UNWEER: 08/463,081
FILING DATE: 5-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATCHORIN Release #1.0,
SOFTWARE: Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/652,446
FILING DATE:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (213) 489-4210 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 08/461,379
FILING DATE: 5-JUN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/739,523
FILING DATE: 29-OCT-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Viviana Amzel, Ph. D.
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: FP.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 622-7700
                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 313 amino acid
                                                                                                                                                                                                                                                                            MOLECULE TYPE:
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                          STRANDEDNESS:
TOPOLOGY: n.a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: EP App. # 96921319 FILING DATE: 5-JAN-1998
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   ERPEFVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180
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California
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Pred. No. 1.6e-159;
0; Mismatches 2;
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US-09-644-450-8
; Sequence 8, Application US/09644450
; Patent No. 6383791
; GENERAL INFORMATION:
; APPLICANT: Kapeller, Rosana
; TITLE OF INVENTION: NOVEL MOLECULES OF THE
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: 03580/175631
; CURRENT APPLICATION NUMBER: US/09/644,450
; CURRENT FILING DATE: 2000-08-23
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US-09-237-543-8
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; APPLICANT: Kapeller, Rosana
; TITLE OF INVENTION: NOVEL MOLECULES OF THE HX
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: 055800/175631
; CURRENT APPLICATION NUMBER: US/09/237,543A
; CURRENT FILING DATE: 199-01-26
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 8
; SEQ ID NO 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; LENGTH: 313
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-09-237-543-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 98.0
Best Local Similarity 97.1
Matches 304; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                         ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI
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                                                                                      PFEHDEEIVKGQVYFRQRVSSECQHLIRWCLSLRPSDRPSFEEIQNHPWMQDVLLPQATA
                                                                                                                PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300
                                                                                                                                                                               ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI
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97.1%;
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Pred. No. 2.1e-157;
6; Mismatches 3;
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THE HKID-1-RELATED PROTEIN FAMILY

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APPLICANT: Kapeller, Rosana
TITLE OF INVENTION: NOVEL MOLECULES OF THE HX
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: 035800/175631
CURRENT APPLICATION NUMBER: US/09/237,543A
CURRENT FILING DATE: 1999-01-26
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PATENTI Ver. 2.0
SEQ ID NO 7
SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 11
US-09-237-543-7
US-09-237-543-7
; Sequence 7, Application US/09237543A
; Patent No. 6143540
; Patent INFORMATION:
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; TYPE: PRT
; ORGANISM: Mus musculus
US-09-237-543-7
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SEQ ID NO 8
LENGTH: 313
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Best Local Similarity 93.9
Matches 294; Conservative
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Best Local Similarity 97.1
Matches 304; Conservative
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SOFTWARE: PatentIn Ve
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                                                                                 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD
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                                         ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG
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ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI
                          ERPEPVQDLFDFITERGALQEDLARGFFWQVLEAVRHCHNCGVLHRDIKDENILIDLSRG
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97.1%;
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                                                                                                                                                                                                94.7%; Score 1582; DB 2;
93.9%; Pred. No. 6.2e-152;
tive 10; Mismatches 9;
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Pred. No. 2.1e-157;
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                                                                                                                                                                                                                          Length 313;
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Kapeller, Rosana
TITLE OF INVENTION: MOVEL MOLECULES OF THE
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: 035800/175631
CURRENT APPLICATION NUMBER: US/09/644,450
CURRENT FILING DATE: 2000-08-23
NUMBER OF SEQ ID NOS: 11
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 7
LENGTH: 313
TYPE: PRT
ORGANISM: Mus musculus
US-09-644-450-7
                                                 ; Sequence 41, Application US/07857224B
; Patent No. 5958784
; GENERAL IMPORMATION:
APPLICANT: Benner, Steven A.
; TITLE OF INVENTION: Predicting Folded St.
; NUMBER OF SEQUENCES: 114
; CORRESPONDENCE ADDRESS:
ADDRESSEE: Steven A. Benner
; Correspondence Steven A. Benner
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US-09-644-450-7
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US-07-857-224B-41
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Best Local Similarity
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STREET: Hadlaubstrasse 151
CITY: Zurich
STATE: none
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Switzerland

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RESULT 14
US-09-237-543-2
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; DATE: 1988
US-07-857-224B-41
GENERAL INFORMATION:
APPLICANT: KAPENIC:
TITLE OF INVENTION: NOVEL MOLECULES OF THE HKID-1-RELATED
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: 035800/175631
CURRENT APPLICATION NUMBER: US/09/237,543A
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Best Local Similarity
Matches 242; Conserv
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CLASSIFICATION: 436
PRIOR APPLICATION DATA: none
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION (International) 41 1 632 2830
TELEPHONE: (International) 41 1 262 2437
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CURRENT APPLICATION DATA:
APPLICATION UMBER: US/07/857,22.
PILING DATE: 03/25/92
CLASSIFICATION.
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DESCRIPTION:
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LENGTH: 257
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COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette, 1.4 Mb storage
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JOURNAL: Sc
VOLUME: 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AUTHORS: Hanks, S. K.
AUTHORS: Quinn, A. M.
AUTHORS: Hunter, T.
TITLE: The protein kinase
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TOPOLOGY: linear
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Pred. No. 4.1e-123;
9; Mismatches 3;
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GENERAL INFORMATION:
APPLICANT: Kappeller, Rosana
TITLE OF INVENTION: NOVEL MOLECULES OF THI
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: 035800/175631
CURRENT APPLICATION NUMBER: US/09/644,450
CURRENT FILING DATE: 2000-08-23
NUMBER OF SEQ ID NOS: 11
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
SEQ ID NO 2
LENGTH: 326
TYPE: PRT
ORGANISM: Homo sapiens
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NUMBER OF SEQ ID NOS: 11
SSOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 326
TYPE: PRT
ORGANISM: Homo sapiens
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US-09-644-450-2
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Best Local S
Matches 219
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Matches 219;
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               116 FVLILERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILI 175
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                                                                                cch 67.8%; Score 1133; DB 2; al Similarity 69.3%; Pred. No. 2.1e-106; 219; Conservative 35; Mismatches 52;
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                                                                                                                               MLLSKFGSLAHL-CGFGGVDHLPVKILQPAKADKESFEKAYQVGAVLGSGGFGTVYAGSR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | VCGDIPFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWM--QDV 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FVLILERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILI 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VSDNLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKV--SSGFSGVIRLLDWFERPDS 115
FLLVLERPEPAQDLFDFITERGALDEPLARRFFAQVLAAVRHCHSCGVVHRDIKDENLLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LLPOETAEIHLHSLSP 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VCGDIPFEQDEEILRGRLLFRRRVSPECQQLIRWCLSLRPSERPSLDQIAAHPWMLGADG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FLLVLERPEPAQDLFDFITERGALDEPLARRFFAQVLAAVRHCHSCGVVHRDIKDENLLV
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Pred. No. 2.1e-106;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       THE HKID-1-RELATED PROTEIN FAMILY
                                                                                                                                                                                                                                Length 326;
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Search Job ti	DЬ	ક	В	Ş	망	ફ
Search completed: May 4, 2006, 05:27:21 Job time : 29.6667 secs	299 GAP-ESCDLRLCTLDP 313	294 LLPQETAEIHLHSLSP 309	239 VCGDIPFEQDEEILRGRLLFRRRVSPECQQLIRWCLSLRPSERPSLDQIAAHPWMLGADG 298	236 VCGDIPFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDV 293	179 DLRSGELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSATVWSLGVLLYDM 238	176 DLNRGELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDM 235

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Result
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             Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*

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6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*
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Listing first 45 summaries
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Copyright (c) 1993 - 2006 Biocceleration Ltd.
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US-10-664-421-150
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Sequence 9, Appli
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US-09-971-791-9
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Q	DB S	φ .:	<b>д</b> ъ	9	gb G	9	Db	9	Db	Qy	Query Match Best Local Matches 31	; ORGANISM: H US-09-971-791-9	TYPE: PRT	; SEQ ID NO	; SOFTWARE:		; PRIOR A	PRIOR A	CURRENT	; FILE RE	; TITLE OF	; APPLICANT:
301 EIHLHSLSPGPSK 313	241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300	241 PFEHDBEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300	181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240	181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240	121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180	121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180	61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120	61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120	1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD 60	1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD 60	Match 100.0%; Score 1670; DB 3; Length 313; Local Similarity 100.0%; Pred. No. 2.2e-143; es 313; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	ORGANISM: Homo sapiens 9-971-791-9		O w		OF SEO ID NOS: 11	APPLICATION NUMBER: 09/237,543	APPLICATION NUMBER: 09/644,450	CURRENT FILING DATE: 2001-10-04	ERENCE: 35800/23885	MI	NT: Laura A. Rudolph-Owen NT: Kvle MacBeth

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RESULT 3
US-10-394-322A-52
Sequence 52, Application US/10394322A
Sequence 52, Application US/10394322A
Publication No. US20030232391A1
GENERAL INFORMATION:
APPLICANT: SUNESIS PHARMACEUTICALS, INC.
APPLICANT: Prescott, John C.
TITLE OF INVENTION: IDENTIFICATION OF KINASE INHIBITORS
FILE REPERENCE: 39750-0006 US
CURRENT APPLICATION NUMBER: US/10/394,322A
CURRENT FILING DATE: 2003-03-20
PRIOR APPLICATION NUMBER: US 60/366,892
PRIOR APPLICATION NUMBER: US 60/366,892
PRIOR APPLICATION NUMBER: US 60/366,892
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PRIOR APPLICATION N
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CURRENT FILING DATE: 2002-02-21
PRIOR APPLICATION NUMBER: 60/289,813
PRIOR FILING DATE: 2001-02-21
NUMBER OF SEO ID NOS: 38
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 18
SEQ ID NO 18
LENGTH: 313
TYPE: PRT
ORGANISM: Homo sapiens
US-10-081-119-18
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Best Local Similarity
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APPLICANT: Jefferson, Anne B.
APPLICANT: Chan, Vivien W.
TITLE OF INVENTION: TTX in Diagnosis and as
TITLE OF INVENTION: Target in Cancer
FILE REFERENCE: 16932.002
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Pred. No. 2.2e-143;
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Matches 313; Conserv
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RESULT 4

US-10-348-081-13

Sequence 13, Application US/10348081

Publication No. US20040038246A1

GENERAL INFORMATION:
APPLICANT: KORN, Marcus
APPLICANT: MUELLER, Guenter
APPLICANT: SCHNEIDER, Rudolf
APPLICANT: TSCHANK, Georg
TITLE OF INVENTION: PHM-3 KINASE AS A TARGET FOR TYPE 2 DIABETES MELLITUS
FILE REFERENCE: DEAV2002/0004 US NP
CURRENT FILING DATE: 2003-01-21

NUMBER OF SEQ ID NO.13

SEQ ID NO.13

LENGTH: 313

TYPE: PRT
COLUMN US OF SERVING SE
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; LENGTH: 313
; TYPE: PRT
; ORGANISM: Homo s
US-10-664-421-1
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APPLICANT: MILBURN, MICHAEL V.
APPLICANT: MILBURN, MICHAEL V.
TITLE OF INVENTION: CRYSTAL STRUCTURE OF PIM-1 KINASE
FILE REFERENCE: 039363/0703
CURRENT APPLICATION NUMBER: US/10/664,421
CURRENT FILING DATE: 2003-09-16
PRIOR APPLICATION NUMBER: 60/412,341
PRIOR APPLICATION NUMBER: 60/412,341
PRIOR APPLICATION NUMBER: 60/412,341
PRIOR FILING DATE: 2002-09-20
PRIOR FILING DATE: 2002-09-16
PRIOR FILING DATE: 2002-09-16
NUMBER OF SEQ ID NOS: 169
                                                                                                                                                   US-10-664-421-150
                                                                                                                                                                         RESULT 6
Sequence 150, Application US/10664421
Publication No. US20040142864A1
GENERAL INFORMATION:
APPLICANT: BREMER, RYAN
APPLICANT: KUMAR, ABHINAV
APPLICANT: KUMAR, ABHINAV
APPLICANT: MANDIYAN, VALSAN
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APPLICANT: BRAHIM, PRAE
APPLICANT: KUMAR, ABHINA
APPLICANT: MANDIYAN, VAL
APPLICANT: MILBURN, MICH
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Best Local Similarity 100.0%;
Matches 313; Conservative 0
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Pred. No. 2.2e-143;
0; Mismatches 0; Indels 0
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; SEQ ID NO 2
; LENGTH: 313
; TYPB; PRT
; ORGANISM: Homo sapiens
US-10-705-757-2
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TITLE OF INVENTION: CRYSTAL STRUCTURE OF PIN
FILE REFERENCE: 039363/0703
CUURRENT APPLICATION NUMBER: US/10/664,421
CURRENT FILING DATE: 2003-09-16
PRIOR APPLICATION NUMBER: 60/412,341
PRIOR FILING DATE: 2002-09-20
PRIOR APPLICATION NUMBER: 60/411,398
PRIOR FILING DATE: 2002-09-16
NUMBER OF SEQ ID NOS: 169
SOFTWARE: Patentin Ver. 3.2
SEQ ID NO 150
LENGTH: 313
TYPE: PRT
ORGANIAN: Homo sapiens
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Publication No. US20040146942A1
GENERAL INFORMATION:
                                   Query Match
Best Local Similarity
Matches 313; Conserva
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TITLE OF INVENTION: SCREENING METHOD USING PIM1-KINASE (
FILE REFERENCE: 029310.52818US
CURRENT APPLICATION NUMBER: US/10/705,757
CURRENT FILING DATE: 2003-11-12
PRIOR APPLICATION NUMBER: PC7/EP02/05234
PRIOR FILING DATE: 2002-05-13
PRIOR FILING DATE: 2002-05-13
PRIOR APPLICATION NUMBER: DE 101 23 055.9
PRIOR PILING DATE: 2001-05-11
NUMBER: OF SEQ ID NOS: 11
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                                     100.0%; Score 1670; DB 4; ilarity 100.0%; Pred. No. 2.2e-143; Conservative 0; Mismatches 0;
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; SEQ ID NO 9
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-377-268-9
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US-10-377-268-9
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PRIOR FILING DATE: 2003-01-02
PRIOR APPLICATION NUMBER: 60/360,651
PRIOR FILING DATE: 2002-02-28
PRIOR APPLICATION NUMBER: 60/411,398
PRIOR FILING DATE: 2002-09-16
PRIOR APPLICATION NUMBER: 60/412,341
PRIOR APPLICATION NUMBER: 60/412,341
PRIOR FILING DATE: 2002-09-20
NUMBER OF SEO ID NOS: 38
SOFTWARE: Patentin Ver. 2.1
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Best Local S
Matches 313
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APPLICANT: MILBURN, MICHAEL VANCE
TITLE OF INVENTION: METHOD FOR THE DESIGN OF MOLECULAR SCAFFOLDS AND LIGANDS
FILE REFERENCE: 039363/0303
CURRENT APPLICATION NUMBER: US/10/377,268
CURRENT FILING DATE: 2003-02-28
CURRENT FILING DATE: 2003-02-28
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 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA
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                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                               100.0%; Score 1670; DB 4;
100.0%; Pred. No. 2.2e-143;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                          DB 4; Length 313;
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Sequence 18, Application US/10951406
; Publication No. US20050059630A1
; GENERAL INFORMATION:
 APPLICANT: Reinhard, Christoph
 APPLICANT: Jefferson, Anne B.
 APPLICANT: Jefferson, Anne B.
 APPLICANT: Chan, Vivien W.
 TITLE OF INVENTION: TTK in Diagnosis and as
 TITLE OF INVENTION: Target in Cancer
 FILE REFERENCE: 16932.002
; CURRENT APPLICATION NUMBER: US/10/951,406
                                                                                                                                      RESULT 10
US-10-951-406-18
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; ORGANISM: Homo
US-10-951-389-18
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APPLICANT: Reinhard, Christoph
APPLICANT: Jefferson, Anne B.
APPLICANT: Chan, Vivien W.
TITLE OF INVENTION: TTK in Diagnosis and as a TITLE OF INVENTION: TTK in Cancer
FILE OF INVENTION: Target in Cancer
FILE REFERENCE: 16932.002
CURRENT APPLICATION UNMBER: US/10/951,389
CURRENT FILING DATE: 2004-09-27
PRIOR APPLICATION NUMBER: US/10/081,119
PRIOR APPLICATION NUMBER: US/10/081,119
PRIOR APPLICATION NUMBER: 60/289,813
PRIOR FILING DATE: 2002-02-21
PRIOR FILING DATE: 2001-02-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 313; Conservative 0
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                                         EIHLHSLSPGPSK 313
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                                                                                                                                                                                   PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300
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EIHLHSLSPGPSK 313
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Pred. No. 2.2e-143;
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CURRENT APPLICATION NUMBER: US/10/951,477
CURRENT FILING DATE: 2004-09-27
PRIOR APPLICATION NUMBER: US/10/081,119
PRIOR FILING DATE: 2002-02-21
PRIOR APPLICATION NUMBER: 60/289,813
PRIOR FILING DATE: 2001-02-21
NUMBER OF SEQ ID NOS: 38
SOFTWARE: FREESEQ for Windows Version 4.0
SEQ ID NO 18
LENGTH: 313
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PRIOR APPLICATION NUMBER: US/10/081,119
PRIOR FILING DATE: 2002-02-21
PRIOR APPLICATION NUMBER: 60/289,813
PRIOR FILING DATE: 2001-02-21
NUMBER OF SEQ ID NOS: 38
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 18
LENGTH: 313
TYPE: PRT
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                                                                                                                       ; TYPE: PRT ; ORGANISM: Homo sapiens US-10-951-477-18
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US-10-951-477-18
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US-10-951-406-18
                                                                                                                                                                                                                                                                                                                                          Sequence 18, Application US/10951477

Publication No. US20050063974A1

GENERAL INFORMATION:

APPLICANT: Reinhard, Christoph
APPLICANT: Jefferson, Anne B.
APPLICANT: Chan, Vivien W.

TITLE OF INVENTION: TTK in Diagnosis and as a Therapeutic
TITLE OF INVENTION: Target in Cancer
FILE REFERENCE: 16932.002
                                                                     Query Match
Best Local Similarity
                                                       Matches
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Best Local :
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                                                       313;
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                                                       Conservative
                                                100.0%; Score 1670; DB 5;
100.0%; Pred. No. 2.2e-143;
tive 0; Mismatches 0;
                                                                                  Length 313;
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; LENGTH: 313
; TYPE: PRT
; ORGANISM: Homo s
US-10-977-087-18
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APPLICANT: Khoja, Hamiduddin
APPLICANT: Khoja, Hamiduddin
APPLICANT: Shyamala, Venkatakrishna
TITLE OF INVENTION: GENE PRODUCTS DIFFERENTI
TITLE OF INVENTION: AND THEIR METHODS OF US
FILE REFERENCE: 2300-21986
CURRENT APPLICATION NUMBER: US/10/977,087
CURRENT FILING DATE: 2004-10-28
PRIOR APPLICATION NUMBER: 10/081,119
PRIOR APPLICATION NUMBER: 60/271,254
PRIOR APPLICATION NUMBER: 60/271,254
PRIOR APPLICATION NUMBER: 10/360,848
PRIOR APPLICATION NUMBER: 10/360,848
PRIOR APPLICATION NUMBER: 09/570,593
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US-10-977-087-18
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Publication No. US20050130926A1
GENERAL INFORMATION:
APPLICANT: Reinhard, Christoph
APPLICANT: Jefferson, Anne B.
                                                                                                                                                          SOFTWARE: FastSEQ
SEQ ID NO 18
LENGTH: 313
Query Match 100.0%; Score 1670; DB 5; Best Local Similarity 100.0%; Pred. No. 2.2e-143; Matches 313; Conservative 0; Mismatches 0;
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APPLICANT:
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                                                                                                                                                                                                                                                                          PRIOR FILING DATE: 2003-10-30
                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 09/626,301
FILING DATE: 2000-07-25
APPLICATION NUMBER: 60/148,936
FILING DATE: 1999-08-13
                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 60/145,612
                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 10/763,692 FILING DATE: 2004-01-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 60/134,112 FILING DATE: 1999-05-14
                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 10/698,959
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                                          Length 313;
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GENERAL ANTICATION.

APPLICANT: BREMER, RYAN E.

APPLICANT: BREMER, RYAN E.

APPLICANT: BREMER, RYAN E.

APPLICANT: HURT, CLARENCE R.

APPLICANT: HURT, CLARENCE R.

APPLICANT: IBRAHIM, PRABHA L.

APPLICANT: ZUCKERMAN, REBECCA L.

TITLE OF INVENTION: MOLECULAR SCAFFOLDS FOR KINASE LIGAND DEVELOPMENT FILE REFERENCE: 039363-1702

CURRENT APPLICATION NUMBER: US/10/941,635

CURRENT FILING DATE: 2004-09-15

PRIOR APPLICATION NUMBER: 60/503,277

PRIOR APPLICATION NUMBER: 60/503,277

PRIOR FILING DATE: 2003-09-15

NUMBER OF SEO ID NOS: 167

SOFTWARE: Patentin Ver. 3.2

SEO ID NO 1

LENGTH: 313

TYPE: PRI
ORGANISM: HOMO sapiens

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US-10-941-635-1
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Publication No. US20050164300A1
GENERAL INFORMATION:
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 Sequence 22, Application US/10620052A
Publication No. US20040126784A1
GENERAL INFORMATION:
APPLICANT: Hitoshi, Yasumichi
APPLICANT: Jenkins, Yonchu
APPLICANT: Markottsov, Vadim
APPLICANT: Rigel Pharmaceuticals, Ir
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Jenkins, Yonchu
Markovtsov, Vadim
Rigel Pharmaceuticals, Inc.
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GENERAL INFORMATION R.

APPLICANT: ARTIS, DEAN R.

APPLICANT: ARTIS, DEAN R.

APPLICANT: GILLETTE, SAMUEL J.

APPLICANT: GILLETTE, SAMUEL J.

APPLICANT: IBRAHIM, PRABHA L.

APPLICANT: ZUCKERMAN, REBECCA L.

TITLE OF INVENTION: MOLECULAR SCAFFOLDS FOR KINASE LIGAND DEVE

FILE REFERENCE: 039363-1702

FULL REFERENCE: 039363-1702

CURRENT APPLICATION NUMBER: US/10/941,635

CURRENT APPLICATION NUMBER: 00/503,277

PRIOR APPLICATION NUMBER: 60/503,277

PRIOR APPLICATION NUMBER: 60/503,277

PRIOR FILING DATE: 2003-09-15

PRIOR FILING DATE: 2003-09-15

SOFTWARE: PATENTING DATE: 203-09-15

SOFTWARE: PATENTING DATE: 203-09-15

SOFTWARE: PATENTING DATE: 203-09-15

LENGTH: 313
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Best Local Similarity 100.0%;
Matches 313; Conservative (
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Pred. No. 2.2e-143;
D; Mismatches 0;
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TITLE OF INVENTION: Modulators of Cellular Proliferation
FILE REFERENCE: 021044-004010US
CURRENT APPLICATION NUMBER: US/10/620,052A
CURRENT FILING DATE: 2003-07-14
PRIOR APPLICATION NUMBER: US 60/395,443
PRIOR FILING DATE: 2002-07-12
NUMBER OF SEQ ID NOS: 78
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 22
LENGTH: 313
TYPE: PRT
ORCANISM: Homo sapiens
FEATURE:
COTHER INFORMATION: PIM1 oncogene serine threonine kinase
US-10-620-052A-22
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Search completed: May 4, 2006, 05:32:05 Job time: 94.6667 secs
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                                                                                                                                                                                                                                       ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180
                                                                                                                                                                                                                                                                                                 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120
                                                                             EIHLHSLSPGPSK 313
                                                                                                                                       PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300
                                                            EIHLHSLSPGPSK 313
                                                                                                                      PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300
                                                                                                                                                                                                                                                                                                                                                                                                                    99.2%; Score 1657; DB 4; Length 313; ilarity 99.4%; Pred. No. 3.3e-142; Conservative 0; Mismatches 2; Indels
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# November 2005

available for processing searches. reduce the amount of time required for their daily updates. This results in more machine time being generate two sets of results each. The Published\_Applications databases have been split into two parts to Published\_Applications Nucleic Acid and Published\_Applications Amino Acid database searches now

applications make up the Published Applications Main databases. Newly published applications will appear in the Published\_Applications\_New databases; older published

Searches run against Amino Acid Published\_Applications produce two sets of results, with the extensions .rapbm (Published\_Applications\_AA\_Main) and .rapbn (Published\_Applications\_AA\_New). .rnpbm (Published\_Applications\_NA\_Main) and .rnpbn (Published\_Applications\_NA\_New). Searches run against Nucleic Acid Published\_Applications produce two sets of results, with the extensions

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Maximum
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence:
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1: /SIDSS/ptodata/2/pubpaa/US06_NEW_PUB.pep1:*

2: /SIDSS/ptodata/2/pubpaa/US06_NEW_PUB.pep:*

3: /SIDSS/ptodata/2/pubpaa/US07_NEW_PUB.pep:*

4: /SIDSS/ptodata/2/pubpaa/US07_NEW_PUB.pep:*

5: /SIDSS/ptodata/2/pubpaa/US09_NEW_PUB.pep:*

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7: /SIDSS/ptodata/2/pubpaa/US09_NEW_PUB.pep:*

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10: /SIDSS/ptodata/2/pubpaa/US11_NEW_PUB.pep:*

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length: 2000000000
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Copyright (c) 1993 - 2006
           BB
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B US-10-511-937-9982

9 US-10-501-841-32

9 US-10-505-928-694

9 US-10-505-928-694

9 US-10-505-928-694

9 US-11-0501-035-357

10 US-11-087-099-9816

10 US-11-087-099-911500

11 US-11-087-099-3150

11 US-11-087-099-3612

12 US-11-087-099-3612

13 US-11-087-099-3612

14 US-11-087-099-3612

15 US-11-087-099-3612

17 US-11-087-099-3612

18 US-10-784-004-435

18 US-10-784-004-951

18 US-10-501-841-37

18 US-10-501-841-37
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US-10-501-841-40
US-11-103-065-2
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Biocceleration Ltd
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Sequence 373, App Sequence 40, Appl Sequence 2, Appli Sequence 74, Appl Sequence 32, Appl Sequence 357, App Sequence 357, App Sequence 11, Appl Sequence 72, Appl Sequence 1130, App Sequence 11500, A Sequence 397, App Sequence 3120, App Sequence 3120, App Sequence 397, App Sequence 397, App Sequence 397, App Sequence 3120, App Sequence 3130, App Sequence 3130, App Sequence 3130, App Sequence 37, Appl Sequence 67, Appl
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US-10-784-004-373
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### ALIGNMENTS

Application US/10784004 o. US20060084066A1

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APPLICANT: Biogen Idec
TITLE OF INVENTION: Surrogate Markers of Pain
FILE REFERENCE: 08201.6029-00000
CURRENT APPLICATION NUMBER: US/10/784,004
CURRENT FILING DATE: 2004-02-20
NUMBER OF SEQ ID NOS: 1251
SOPTWARE: Patentin version 3.2
SEQ ID NO 373
LENGTH: 455
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                          ; ORGANISM: rat
US-10-784-004-373
                                                                                                                                                                                                                                                                                                                        Query Match 67.6
Best Local Similarity 72.2
Matches 213; Conservative
                                                                308
 368
                                                                                              176
                                                                                                                              248
                                                                                                                                                             116
                                                                                                                                                                                               189
                                                                                                                                                                                                                                                           130 MILSKFGSLAHL-CGPGGVDHLPVKILQPAKADKESFEKVYQVGAVLGSGGFGTVYAGSR
                                                                                                                                                                                                              58 VSDNLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKV--SSGFSGVIRLLDWFERPDS 115
                                                                                                                                                                                                                                                                              1 MLLSKINSLAHLRAAP--CNDLHATKLAPGK-EKEPLESQYQVGPLLGSGGFGSVYSGIR
FVLILERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILI
                                                                                                                              FLLVLERPEPAQDLEDFITERGALDEPLARRFFAQVLAAVRHCHNCGVVHRDIKDENLLV
                                                                                                                                                                                               IADGLPVAVKHVVKERVTEWGSL-GGMAVPLEVVLLRKVGAAGGARGVIRLLDWFERPDG
                                                                                                                                                                                                                                                                                                                                           67.6%; Score 1128.5; DB 9; 72.2%; Pred. No. 2.5e-88;
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                                                                                                                                                                                                                                                                                                                             Mismatches
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                                                                                                                                                                                                                                                                                                                                                            455;
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APPLICANT:
APPLICANT:

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APPLICANT: Cappel, Condition David
APPLICANT: Wang, Aljun
APPLICANT: Carter, Lauren
APPLICANT: Carter, Lauren
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnatic Office of Invention: and Therapy of Hematological Malignancies
FILE REFERENCE: 014058-014402PC
CURRENT APPLICATION NUMBER: US/10/501,841
CURRENT FILING DATE: 2004-07-14
PRIOR APPLICATION NUMBER: US 10/057,475
PRIOR APPLICATION NUMBER: WO 70/57,475
PRIOR APPLICATION NUMBER: WO 70/57,475
PRIOR REPLICATION NUMBER: WO PCT/US03/02353
PRIOR FILING DATE: 2003-01-22
NUMBER OF SEQ ID NOS: 124
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 40
LENGTH: 311
TYPE: PRT
ORGANISM: Homo sapiens
CURRENT APPLICATION NUMBER: US/11/103,065
CURRENT FILING DATE: 2005-04-11
PRIOR APPLICATION NUMBER: US/10/184,563
PRIOR FILING DATE: 2002-06-27
PRIOR APPLICATION NUMBER: 60/301,702
PRIOR APPLICATION NUMBER: 60/301,702
PRIOR FILING DATE: 2001-06-28
NUMBER OF SEQ ID NOS: 7
SOFTWARE: F88tSEQ for Windows Version 4.0
SEQ ID NO 2
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                                                                                                                                                                                                                                        Sequence 2, Application US/11103065
Publication No. US20050282189A1
GENERAL INFORMATION:
APPLICANT: Meyers, Rachel E., Lora, Jose M.
TITLE OF INVENTION: 2150, Human Protein Kinase Family
TITLE OF INVENTION: Member and Uses Therefor
FILE REFERENCE: MPI2001-137PIRNM
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Best Vecal Similarity
Matches 167; Conserv
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APPLICANT: Algate, Paul A.
APPLICANT: Mannion, Jane
APPLICANT: Clapper, Jonathan David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       82 LEVALLWKVGAGGGHPGVIRLLDWFETQEGFMLVLERPLPAQDLFDYITEKGPLGEGPSR 141
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CFFGQVVAAIQHCHSRGVVHRDIKDENILIDLRRGCAKLIDFGSGALLHDEPYTDFDGTR
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APPLICANT: MORYIG, MacDonald
APPLICANT: ROSENBERG, Steven
ITITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
ITITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
ITITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
ITITLE OF INVENTION: MUTHORISH TRANSPLANT REJECTION
FILE REFERENCE: 506612000104
CURRENT APPLICATION NUMBER: US/10/511,937
CURRENT FILING DATE: 2004-019
PRIOR APPLICATION NUMBER: PCT/US2003/012946
PRIOR APPLICATION NUMBER: PCT/US2003/012946
PRIOR APPLICATION NUMBER: US 10/131,831
PRIOR APPLICATION NUMBER: US 10/131,831
PRIOR APPLICATION NUMBER: US 10/325,899
PRIOR FILING DATE: 2002-04-24
PRIOR FILING DATE: 2002-12-20
NUMBER OF SEQ ID NOS: 3117
SOPTWARE: PatentIn version 3.2
SEQ ID NO 2982
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; ORGANISM: Homo sapiens
US-11-103-065-2
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                                                                                                                                                                                                                Query Match 51.7%; Score 864; DB 8; Best Local Similarity 61.3%; Pred. No. 5.5e-66; Matches 163; Conservative 37; Mismatches 64
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Best Local Similarity
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APPLICANT:
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TYPE: PRT
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                                88 MEVVLLKKVSS--GFSGVIRLLDWFERPDSFVLILERPEPVQDLFDFITERGALQEELAR 145
                                                                                                                                        28 GKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSDNLPVAIKHVEKDRISDWGELPNGTRVP
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     82 LEVALLWKVGAGGGHPGVIRLLDWFETQEGFMLVLERPLPAQDLFDYITEKGPLGEGPSR
                                                                                                          22 GKDREAFEAEYRLGPLLGKGGFGTVFAGHRLTDRLQVAIKVIPRNRVLGWSPLSDSVTCP 81
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RESULT 6
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US-10-501-841-32
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Best Local S
Matches 163
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 32, Application US/10501841 Publication No. US20060084055A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis TITLE OF INVENTION: and Therapy of Hematological Malignancies FILE REFERENCE: 0.14058-014402PC
CURRENT APPLICATION NUMBER: US/10/501,841
CURRENT FILING DATE: 2004-07-14
PRIOB APPLICATION NUMBER: US 10/057,475
PRIOR APPLICATION NUMBER: US 10/057,475
PRIOR FILING DATE: 2002-01-22
PRIOR PPLICATION NUMBER: WO PCT/US03/02353
PRIOR FILING DATE: 2003-01-22
NUMBER OF SEQ ID NOS: 124
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ORGANISM: Homo sapiens
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                                                                                                                                                   202
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                                                                                                              LIRWCLALRPSDRPTFEEIQNHPWMQ 291
                                                                                                                                                                                                                                                                              LEVALLWKVGAGGGHPGVIRLLDWFETQEGFMLVLERPLPAQDLFDYITEKGPLGEGPSR
                                                                                                                                                                                                                                                                                                           MEVVILKKVSS--GFSGVIRLLDWFERPDSFVLILERPEPVQDLFDFITERGALQEELAR 145
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                                                                                                                                                   VYSPPEWISRHQYHALPATVWSLGILLYDMVCGDIPFERDQEILEAELHFPAHVSPDCCA 261
                                                                                                                                                                              VYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDIPFEHDEEIIRGQVFFRQRVSSECQH
                                                                                   LIRRCLAPKPSSRPSLEEILLDPWMQ 287
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Carter, Lauren
McNeill, Patricia Dianne
Corixa Corporation
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61.3%; Pred. No. 5.5e-66;
tive 37; Mismatches 64
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Best Local Similarity
Matches 98; Conserv
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SEQ ID NO 74
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Stone, David
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; LENGTH: 256
; TYPE: PRT
; ORGANIAM: Artificial Sequence
; PEATURE:
; OTHER INFORMATION: Description of Artificial
; OTHER INFORMATION: domain Consensus Sequence
US-10-877-346-74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: US/09/964,956
PRIOR FILLING DATE: 2001-09-26
PRIOR PELICATION NUMBER: 60/235,631
PRIOR FILLING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: 60/235,633
PRIOR FILLING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: 60/235,808
PRIOR APPLICATION NUMBER: 60/235,064
PRIOR FILLING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: 60/236,064
PRIOR APPLICATION NUMBER: 60/236,064
PRIOR APPLICATION NUMBER: 60/236,065
PRIOR APPLICATION NUMBER: 60/236,065
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PRIOR APPLICATION NUMBER: 60/237,434
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/238,321
PRIOR FILING DATE: 2000-10-05
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CURRENT APPLICATION NUMBER: US/10/877,346
CURRENT FILING DATE: 2004-06-25
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APPLICANT: Spyrek, Kimberly A
APPLICANT: Leach, Martin D
APPLICANT: Shimkets, Richard A
TITLE OF INVENTION: Novel Proteins and Nucleic Acids Encoding Same
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: 60/236,135
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APPLICATION NUMBER: 60/236,066
FILING DATE: 2000-09-27
                                                                                                                               HCHNCGVLHRDIKDENILIDLNRGELKLIDFGSGALLKDTVY---TDFDGTRVYSPPEWI
                        RYHRYHGRSAAVWSLGILLYDMVCGDIPF---EHDEEIIRGQVFFRQRV------SSECQ
EGRGYSSK-VDVWSLGVILYELLTGKLPFPGIDPLEELFRIKERPRLRLPLPPNCSEELK
                                                                                                   YLHSRGIVHROLKPENILLDEN-GTVKIADFGLARKLESSSYEKLTTFVGTPEYMAPEVL
                                                                                                                                                                                                     --HPNIVRLLGVFEEDDHLYLVMEYMEG-GDLFDYLRRNGLLLSEKEAKKIALQILRGLE 112
                                                                                                                                                                                                                                                   SGFSGVIRLLDWFERPDSFVLILERPEPVQDLFDFITERG-ALQEELARSFFWQVLEAVR
                                                                                                                                                                                                                                                                                                           YELGEKLGSGAFGKVYKGKHKDTGEIVAIKILKKRSLSE-----KKKRFLREIQILRRLS
                                                                                                                                                                                                                                                                                                                                                         YQVGPLLGSGGFGSVYSGIRVSDNLFVAIKHVEKDRISDWGELFNGTRVFMEVVLLKKVS
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Smithson, Glennda
Millet, Isabelle
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Grosse, William M
Alsobrook II, John
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                                                                                                                                                                                                                                                                                                                                                                                                             23.0%; Score 384.5;
37.0%; Pred. No. 2.56
tive 46; Mismatches
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nes 98;
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PRIOR APPLICATION NUMBER: US 60/363,019
PRIOR FILING DATE: 2002-03-07
NUMBER OF SEQ ID NOS: 866
SOFTWARE: PATENTIN 3.2
SEQ ID NO 690
LENGTH: 661
TYPE: PRT
ORGANISM: Homo sapiens
; ORGANISM: Homo sapiens US-10-501-035-357
                                                                                                                                                                                                                                                                                                                                                                     US-10-501-035-357; Sequence 357, A; Publication No.
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                                      NUMBER OF SEQ ID NOS: 795
SOFTWARE: PatentIn version 3.2
SEQ ID NO 357
LENGTH: 950
TYPE: PRT
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Best Local :
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                                                                                                                                              APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: IDENTIFICATION OF POLYNUCLEOTIDES AND POLYPEPTIDE FOR PREDICTING
TITLE OF INVENTION: AND/OR PROTEIN TYROSINE KINASE PATHWAYS
TITLE OF INVENTION: AND/OR PROTEIN TYROSINE KINASE PATHWAYS
FILE REFERENCE: D0185 PCT
CURRENT APPLICATION NUMBER: US/10/501,035
CURRENT FILING DATE: 2004-07-09
PRIOR APPLICATION NUMBER: US 60/350,061
PRIOR FILING DATE: 2002-01-18
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CURRENT APPLICATION NUMBER: US/10/505,928
CURRENT FILING DATE: 2004-08-27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             151 VLEAVRHCHNCGVLHRDIKDENILIDLNRGELKLIDFG-SGALLKDTVYTDFDGTRVYSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        105 EIMS--SLNHPHIISIYEVFENKDKIVIIMEYASK-GELYDYISERRRLSERETRHFFRQ
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US-11-241-056-11
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Publication No. US20060024807A1
GENERAL INFORMATION:
APPLICANT: Immunex Corporation
APPLICANT: Bird, Timothy A.
APPLICANT: Virca, G. Duke
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn version 3.1 SEQ ID NO 11
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Best Local
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Anderson, Dirk M.
TITLE OF INVENTION: NOVEL MURINE AND HUMAN KINASES
FILE REFERENCE: 2923-US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 631
TYPE: PRT
ORGANISM: Mus musculus
                                                                                    196
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                                  244 HDE-----EIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWM 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           271 LALRPSDRETFEEIQNHPWM-----QDVLLPQE 298
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                                                                                                                                                                                                                125 PVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRGELKL 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  276 LVLDPSKRLTIAQÍKEHKWMLIEVPVQRPVLYPQE 310
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                                                                                                                                                                                                                                                                                                       65 AIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLILERPE 124
                                                                                                                                                                                                                                                                                                                                                   24 ARPLADGLIKSPKPLMKKQAVKRHHKHNLRHRYEFLETLGKGTYGKVKKA-RESSGRLV
                                                                                                                                                                                                                                                                                                                                                                                            22 ATKLAPGKEKEP-------LESQYQVGPLLGSGGFGSVYSGIRVSDNLPV
                                                                                                                                                                                                                                                                                                                                                                                                                                          98;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              89;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
GQDHKTLVKQISNGAYREPPKPSDAC-GLIRWLLMVNPTRRATLEDVASHWWV
                                                                                    ADFGLSNLYHKGKFLOTFCGSPLYASPEIVNGKPYVGPEVDSWSLGVLLYILVHGTMPFD
                                                                                                                              IDFG-SGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDIPFE
                                                                                                                                                                         R-GDLYDYISERPRLSERDARHFFRQIVSALHYCHQNGIVHRDLKLENILLDAN-GNIKI
                                                                                                                                                                                                                                                              AIKSIRKDKIKDEQDL---LHIRREIEIMS--SLNHPHIIAIHEVFENSSKIVIVMEYAS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CHNCGVLHRDIKDENILIDLNRGELKLIDFGSGALLKD-TVYTDFDGTRVYSPPEWIRYH 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SGFSGVIRLLDWFERPDSFVLILERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRH 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YDIEGTLGKGNFAVVKLGRHRITKTEVAIKIIDKSQL----DAVNLEKIYREVQIMKMLD 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QYEGPOLDIWSMGVVLYVLVCGALPFDGPTLPILRQRVLEGRFRIPYFMSEDCEHLIRRM 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CHGRKIVHRDLKAENLLLD-NNMNIKIADFGFGNFFKSGELLATWCGSPPYAAPEVFEGQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                     22.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 376; DB 9; Length 950; Pred. No. 6.6e-24;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 368.5; DB 11;
Pred. No. 1.7e-23;
6; Mismatches 116;
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Sequence 9816, Application US/11087099
Publication No. US20060041961A1
GENERAL INFORMATION:
APPLICANT: Abad, Mark S. et al.
TITLE OF INVENTION: Genes and Uses for Plant FILE REFERENCE: 38 21 (53450) EP
CURRENT APPLICATION NUMBER: US/11/087,099
CURRENT FILING DATE: 2005-03-22
NUMBER OF SEQ ID NOS: 12464
SEQ ID NO 9816
LENGTH: 504
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US-11-087-099-9816
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Matches
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APPLICANT:
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                    PRIOR
                                               APPLICANT: Shimkets, Richard A
TITLE OF INVENTION: Novel Proteins and Nucleic
FILE REFERENCE: 21402-124
CURRENT APPLICATION NUMBER: US/10/877,346
CURRENT FILING DATE: 2004-06-25
PRIOR APPLICATION NUMBER: US/9964,956
PRIOR FILING DATE: 2001-09-26
PRIOR FILING DATE: 2001-09-26
                                                                                                                                                                                                                              APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Gerlach, Valerie L
APPLICANT: MacDougall, John R
APPLICANT: Smithson, Glennda
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                APPLICATION NUMBER: 60/235,631 FILING DATE: 2000-09-27
APPLICATION NUMBER: 60/235,633
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 38 YQVGPLLGSGGFGSVYSGIRVSDNLFVAIKHVEKDRISDWGELFNGTRVFMEVVLLKKVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               65 -- HPHIIRLYEVIETPSDIYVVMEYVKS-GELEDYIVEKGRLQEDEARNFFQQIISGVEY 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         90;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLALRPSDRPTFEEIQNHPWMQ 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LYAGPEVDVWSCGVILYALLCGTLPFD-DENIPNLFKKIKGGIYTLPSHLSSGARELIPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CHNCGVLHRDIKDENILIDLNRGELKLIDFGSGALLKDTVYTDFD-GTRVYSPPEWIRYH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YKLGKTLGIGSFGKVKIAEHALTGHKVAIKILNRRKIKN---LDMEEKVRREIKILRLFM
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Smithson, Glennda
Millet, Isabelle
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                                                                                                                                                                                                                                                                        Ellerman, Karen
Grosse, William M
Alsobrook II, John P
                                                                                                                                                                                                                                                                                                                                                   Millet, Isabe
Stone, David
                                                                                                                                                                                         Kekuda, Ramesh
Spytek, Kimberly A
                                                                                                                                                                                                                          Lepley, Denise M
Burgess, Catherine E
Padigaru, Muralidhara
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                                                                                                                                                                          Leach, Martin D
                                                                                                                                                                                                                                                                                                                                 Gunther, Erik
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 366; DB 11;
Pred. No. 2.1e-23;
1; Mismatches 105;
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                                                                                                                                         Acids
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                                                                                                                                      Encoding
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                                    CURRENT APPLICATION NUMBER: US/11/113,42
CURRENT FILING DATE: 2005-04-21
PRIOR APPLICATION NUMBER: 60/256,704
PRIOR FILING DATE: 2000-12-19
PRIOR FILING DATE: 2000-12-19
PRIOR FILING DATE: 2001-08-10
PRIOR FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: 60/257,314
PRIOR APPLICATION NUMBER: 60/257,314
PRIOR APPLICATION NUMBER: 60/257,314
PRIOR FILING DATE: 2001-08-10
PRIOR FILING DATE: 2001-08-10
PRIOR FILING DATE: 2001-08-10
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                                                                                                                                                                                                                                                                                                         Sequence 183, Applic Publication No. US20 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Ver. SEQ ID NO 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local
                                                                                                                                                                                                                                             APPLICANT: Gangolli et al.
TITLE OF INVENTION: Polypeptides and Nucleic
FILE REFERENCE: 21402-225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Remaining Prior Application data removed - See File Wrapper or PALM NUMBER OF SEQ ID NOS: 127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: 60/237,434 PRIOR FILING DATE: 2000-10-03
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OTHER INFORMATION: Description of Artificial Sequence:
OTHER INFORMATION: Serine/Threoniune protein kinase Consensus
OTHER INFORMATION: Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 256
TYPE: PRT
ORGANISM: Artificial Sequence
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APPLICATION FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 2000-09-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 60/236,066
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            263 CQHLIRWCLALRPSDRPTFEEIQNHPW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       172
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    114 LHSQGIIHRDLKPENILLD-SDGHVKLADFGLAKQLDSGGTLLTTFVGTPEYMAPE-VLL 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             158 CHNCGVLHRDIKDENILIDLNRGELKLIDFGSGALLKD--TVYTDFDGTRVYSPPEWIRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                      229 AKDLIKKLLVKDPEKRLTAEEALEHPF
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                   60/315,617
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Pred. No. 1.2e-
55; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            289
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                                                                                                                                                                                                                                                                  Acids
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APPLICANT: Abad, Mark S. et al.
TITLE OF INVENTION: Genes and Uses for Plant Improvement
FILE REFERENCE: 38-21(5345)B EP
CURRENT APPLICATION NUMBER: US/11/087,099
CURRENT FILING DATE: 2005-03-22
NUMBER OF SEQ ID NOS: 12464
SEQ ID NO 11500
LENGTH: 514
TYPE: PRT
ORGANISM: Lycopersicon esculentum
US-11-087-099-11500
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Matches
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Publication No. US20060041961A1
GENERAL INFORMATION:
                                                                                                                                                  Query Match
Best Local
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Best Local Similarity
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PRIOR FILING DATE: 2001-07-24
PRIOR APPLICATION NUMBER: 60/322,358
PRIOR FILING DATE: 2001-09-14
PRIOR APPLICATION NUMBER: 60/294,075
PRIOR FILING DATE: 2001-05-29
PRIOR FILING DATE: 2001-05-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  114 LHSQGIIHRDLKPENILLD-SDGHVKLADFGLAKQLDSGGTLLTTFVGTPEYMAPE-VLL 171
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                               SGFSGVIRLLDWFERPDSFVLILERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRH
                                                                                                   YQVGPLLGSGGFGSVYSGIRVSDNLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVS
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--HPHIIRLYEVIETPSDIYVVMEYVKS-GELFDYIVEKGRLQEDEARNFFQQIISGVEY
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                                                                   YKLGKTLGIGSFGKVKIAEHTLTGHKVAVKILNRRKIRN---MDMEEKVRREIKILRLFM
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                                                                                                                                 21.3%; Score 356; DB 11; 33.2%; Pred. No. 1.6e-22; ative 54; Mismatches 105;
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Pred. No. 1.2e-23;
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                                                                                                                                                        Sequence 3612, Application US/11087099
Publication No. US20060041961A1
GENERAL INFORMATION:
APPLICANT: Abad, Mark S. et al.
TITLE OF INVENTION: Genes and Uses for Plant Improvement
FILE REFERENCE: 38-21(53450)B EP
CURRENT APPLICATION NUMBER: US/11/087,099
CURRENT FILING DATE: 2005-03-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Abad, Mark S. et al.

TITLE OF INVENTION: Genes and Uses for Plant Improvement
FILE REFERENCE: 38-21(53450)B EP
CURRENT APPLICATION NUMBER: US/11/087,099
CURRENT FILING DATE: 2005-03-22
NUMBER OF SEQ ID NOS: 12464
SEQ ID NO 3997
LENGTH: 512
TYPE: PRT
ORGANISM: Solanum tuberosum
                                                          NUMBER OF SEQ ID NOS: 12464
SEQ ID NO 3612
LENGTH: 514
TYPE: PRT
ORGANISM: Solanum tuberosum
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Matches
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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      192 LYAGPEVDVWSCGVILYALLCGTLPFDDENIPNLFKKIKGGYITLPSHLSAGARDLIPRM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   38 YOVGPLLGSGGFGSVYSGIRVSDNLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVS
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  Score 352;
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Search completed: May 4, 2006, 05:32:56 Job time: 16.3333 secs
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                                               252 LIVDPMKRMTIPEIRLHPWFQ 272
                                   271 LALRPSDRPTFEEIQNHPWMQ 291
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3: geneseqp2000s:*
4: geneseqp2001s:*
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Human PIM	Human cal	Human pro	Human ser	Human HKI	Human ser	Plant ful	ниннл20 р	Colurnix	Human pro	Human kin	Rat prote	PIM1 domi	Mouse Pim	House mou	Mouse Pim	Mus muscu	Murine Pi	Mouse ser	Murine PI	Mouse pro	

### ALIGNMENTS

#### RESULT 1 Homo Pim1; tyrosine threonine kinase; TTK; protein kinase; enzyme; mitotic checkpoint; colon cancer; breast cancer; tumour; cytostatic; human; gene therapy. Reinhard C, Jefferson Human Pim1 21-FEB-2001; 2001US-0271254P 06-SEP-2002 ABP54943; 21-FEB-2002; 2002WO-US005278 WO200268444-A1 13-JAN-2003 ABP54943 standard; protein; 313 (CHIR ) CHIRON CORP 2002-698650/75 sapiens. (first entry) Æ, Chan Æ ≨

Reducing growth of cancer cells comprises reducing Tyrosine Threonine Kinase (TTK) activity, useful in diagnosing and treating disorders with abnormal expression levels and activity of TTK, such as lung, colon, prostate and ovarian cancer.

N-PSDB; WPI;

ABV73989

Disclosure; Page 80-81; 113pp; English.

The present sequence is the protein sequence of human Piml, a protein related to tyrosine threonine kinase (TTK, see ABP54938). TTK polymucleotides and polypeptides of the invention encompass polymucleotides and polypeptides having sequence similarity or sequence identity to human TTK and other genes and gene products related to TTK, such as Piml. The invention is based on the finding that TTK is differentially expressed in various forms of cancer. It provides methods for the identification of cancerous cells, especially breast cancer and colon cancer cells, by detection of expression levels of TTK, as well as

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Best Local Similarity
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                                                                                                                                                                                                                                                                                          HKID-1; serine/threonine kinase; cellular proliferative disorder; differentiative disorder; cancer; haematopoietic neoplastic disorder promyeloid leukaemia; APML; Chronic myelogenous leukaemia; HML; Chronic myelogenous leukaemia; WM; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      diagnostic, prognostic and therapeutic methods. These methods can be used as the basis of rational therapy. Assays for identifying molecules that modulate the activity of these genes in cancers, as well as methods of inhibiting tumour growth by inhibiting the activity of TTK are also
            Modulating levels or activity of HKID-1 polypeptides, a member of serine/threonine kinase superfamily, for treating cancer, by contacting cell expressing the polypeptide with a modulator of the polypeptide.
                                                                                           Kapeller-Libermann R,
                                                                                                                                              26-JAN-1999; 99US-00237543.
23-AUG-2000; 2000US-00644450.
                                                                                                                                                                                      04-OCT-2001; 2001US-00971791.
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Pred. No. 1.4e-154;
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Matches 313;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 313 AA;
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                        EIHLHSLSPGPSK 313
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EIHLHSLSPGPSK 313
                                                                          PFEHDEETIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEETQNHPWMQDVLLPQETA
                                                                                                   PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA
                                                                                                                                                       ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI
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ilarity 100.0%;
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RESULT 3
AAO19788
ID AAO1
XX AAO1
XX AAO1
XX Huma
XX Huma
XX Huma
XX Homo
XX Homo
XX WO20
XX II-M
XX I WO200293173-A2 Human; PIM1 kinase; Human PIM1 kinase 11-AUG-2003 AA019788 13-MAY-2002; 2002WO-EP005234. 21-NOV-2002. 11-MAY-2001; 2001DE-01023055 CHEF ) GRUENENTHAL GMBH Ή standard; Schaefer MK; (first protein; PIM3 kinase; 313 pain; analgesic

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RESULT 4
RABUG11613
ID ABUG6
XX ABUG6
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XX Huma
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XX Homo
XX Homo
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N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        compounds, involving screening candidate compounds for interaction with PIM1 or PIM3 kinase. PIM1 and PIM3 proteins and coding sequences are useful for treating chronic pain, particularly of neuropathic or inflammatory origin (e.g. where associated with diabetes, cancer, AIDS neurodegenerative diseases). The present sequence is human PIM1 kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             chronic pain, by screening conkinase, or related compounds.
(REIN/)
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                                                                                                          06-MAR-2003
                                                                                                                                                                                                                            Human
                                                                                                                                                                                                                                                                                                        ABU61613 standard; protein; 313
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Method for identifying analgesics, useful particularly for treating chronic pain, by screening compounds for interaction with PIM-1 or
                                                                               21-FEB-2002;
                                                                                                                                 US2003045491-A1
                                                                                                                                                             Homo
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DB; ABZ69186.
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) REINHARD C.
) JEFFERSON A L
) CHAN V W.
                                                                                                                                                                                    tyrosine threonine kinase; c checkpoint gene; PIM1.
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                                                                                                                                                                                                                           protein
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100.0%; Pred. No. 1.
tive 0; Mismatches
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Reinhard C,
Jefferson
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N-PSDB; ACA62265 2003-456566/43

normal cell, v is indicative ing cancer in a subject, by comparing expression levels of tyrosine ine kinase polypeptide or polynucleotide in a subject cell and a cell, where an increase in the expression level in the test cell

Disclosure; Page 34-35; 79pp; English.

CC a subject, comprising comparing the expression levels of tyrosine threonine kinase (TTK, a mitotic checkpoint gene) polypeptide or polynucleotide in a test cell obtained from the subject and in a normal connection acid in the test cell compared to that in the normal connectic acid in the test cell compared to that in the normal cell, con rucleic acid in the test cell compared to that in the normal cell condicates the presence of cancer other than ovarian cancer. Also included care reducing growth of a cancerous cell (by contacting a cancerous cell comprising; (i) detecting the activity of a cancerous cell (comprising; (i) detecting the candidate agent cancerous cell contacting a cancerous cell displaying elevated expression of a TTK contacting a cancerous cell displaying elevated expression of a TTK cancerous cell displaying elevated expression of a TTK contacting a cancerous cell displaying elevated expression of a TTK cancerous disease other than ovarian cancer in a contacting a cancerous cell displaying elevated expression of a TTK cancerous cell with a cancerous disease other than ovarian cancer in a contact of expression of TTK encoding polynucleotide in the test cancer cell with prognosis of the polynucleotide in the test cancer cell with prognosis of the polynucleotide in a control non-cancer cell with prognosis of the polynucleotide in the test cancer cell creduces growth of a cancerous cells, identifying a candidate agent that reduces TTK condicative of the prognosis of the polynucleotide in a control non-cancer cell is creduced growth of a cancerous cells, identifying a candidate agent that cancer cell creduces growth of a cancerous cells, identifying a candidate agent that cancer that reduces TTK activity and assessing the prognosis of a cancerous disease other than ovarian cancer) in a subject, or a subject to respond to a particul The invention relates to detecting cancer (other than ovarian can a subject, comprising comparing the expression levels of tyrosine cancer) in

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Query Match Best Local Similarity

100.0%;

Length

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                  PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWWQDVLLPQETA
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PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA
                                                                      ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI
                                                                                                                                          ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG
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Pred. No. 1.4e-154;
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Best Local S
Matches 313
                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence is the protein sequence of the human serine/threonine protein kinase and proto-oncogene, PIM-1. PIM-1 proteins are the paralogues of novel human and murine PIM-3 proteins (see ABR6293; and ABR6293) of the invention, which are therefore expected to be involved in cancer and cell growth regulation. PIM-3 is also involved in the development of insulin resistance and type 2 diabetes mellitus. The invention relates to the use of PIM-3 nucleic acids and proteins in: screening assays for compounds that modulate insulin resistance or type 2 diabetes mellitus (e.g. chromosognal mapping, tissue typing, corrensic biology); predictive medicine (e.g. diagnostic or prognostic assays, monitoring clinical trials, pharmacogenomics); and for the preparing a medicament for the treatment of insulin resistance or type 2 diabetes mellitus (e.g. the preparing and for the preparing a medicament for the treatment of insulin resistance or type 2 diabetes mellitus (e.g. the preparing a medicament for the treatment of insulin resistance or type 2 diabetes mellitus (e.g. the preparing a medicament for the treatment of insulin resistance or type 2 diabetes mellitus (e.g. the preparing a medicament for the treatment of insulin resistance or type 2 diabetes mellitus (e.g. the preparing a medicament for the treatment of insulin resistance or type 2 diabetes mellitus (e.g. the preparing a medicament for the treatment of insulin resistance or type 2 diabetes mellitus (e.g. the preparing a medicament for the treatment of insulin resistance or type 2 diabetes mellitus (e.g. the preparing a medicament for the treatment of insulin resistance or type 2 diabetes mellitus (e.g. the preparing a medicament for the preparing a med
                                                                                                                                                                                                                                                                                                                                                        Sequence 313
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New human or murine PIM-3 DNAs or polypeptides, useful for agent for identifying anti-type 2 diabetes mellitus drugs, treating insulin resistance or type 2 diabetes mellitus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19-JAN-2002; 2002EP-00001401.
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                         ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG
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                                                                                                                                                                                                                                                                     Conservative
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Pred. No. 1.4e-154;
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s (see ABR62932
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         Collined are a vector, a method for identifying a nucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a composition of the perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polynucleotide sequence contact is differentially expressed in neuronal tissue of a first animal compound of a polynucleotide sequence which is differentially expressed in a method for identifying a compound which regulates the expression of a polynucleotide sequence which is differentially compound that regulates the activity of one or more of the composition, a method for identifying a compound that regulates the compound or small molecule that regulates the contivity in an animal of one or more of the polynucleotides, a method for identifying a compound useful in treating composition, a method for identifying a compound useful in treating compositions and a pharmaceutical composition composition the one or more composition in the original activity is useful for preparing a mediament for treating compoint its activity is useful for preparing a mediament for treating compoint its activity is useful for preparing a mediament for treating compoint its activity is useful for preparing a mediament for treating compoints.
                                                                                                                                                                                                                                                                                                                             The invention discloses a composition comprising two or more or human polynucleotides or a polynucleotide which represents derivative or allelic variation of the nucleic acid sequence.
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01-NOV-2001; 2001US-0346382P
26-NOV-2001; 2001US-0333347P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; pain; neuronal tissue; gene therapy; spinal segmental nerve injury; chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Page; 1017pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                     New composition comprising two or more isolated polypeptides, useful preparing a medicament for treating pain in an animal.
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(FARB )
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                                                                                                                                                                                                                                                                                                                                                               The invention discloses a
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BAYER AG.
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   segmental nerve injury
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                                     Identifying ligand binding to inact kinase (T) comprises contacting the contains reactive group at binding kinase-ligand conjugate formation.
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                                                                                                                                                                                                                                                             02-OCT-2003.
                                                                                                                                                                                                                                                                                                                                              Human; protein kinase;
                                                                                                                                            Prescott
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iding site, with ligands and detecting
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Matches 313
                                                                                                                                                                                                     central nervous system; peripheral nervous system; demyelinating polyneuropathy; Guillain-Barre syndrome; chronic inflammatory demyelinating polyneuropathy.
                                                                                                                                                                                                                                                     Human; PRO; immune related disorder; systemic lupus erythematosus; rheumatoid arthritis; osteoarthritis; juvenile chronic arthritis; systemic sclerosis; Sjogren's syndrome; vasculitis; sarcoidosis; systemic acclerosis; Sjogren's autoimmune thrombocyropenia; thyroiautoimmune haemolytic anaemia; autoimmune thrombocyropenia; thyroiautobets mellitus; renal disease; demyelinating disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention relates to a method for identifying a ligand (L), which binds to an inactive conformation of target protein kinase (T). The method involves contacting inactive conformation of (T), which contains or is modified to contain a reactive group at or near a binding site of interest, with one or more ligand candidates capable of covalently bonding to the reactive group thus forming a kinase-(L) conjugate (C). The method is useful for identifying protein kinase inhibitors that preferentially bind to inactive conformation of a target protein kinase. The present sequence is a protein kinase which may be modified via an amino acid substitution, for use in the method of the invention.
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Mismatches 0;
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Matches 313
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                                                                                                             Molecular
G-protein
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     US2004171062-A1
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313; Conservative 0;
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Wu TD;
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                                                                                                             scaffold; nuclear hormone receptor; TNF receptor;
coupled receptor; methyl transferase; ligase; PIM; human
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Best Local Similarity
Matches 313; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention relates to a method of designing a ligand binding to a target molecule. The method involves identifying as molecular scaffolds compounds binding to members of a molecular family, detecting orientation of scaffolds at a binding site of target, and synthesising ligand. The invention is useful for designing drug products and for designing ligand binding to target molecules such as nuclear hormone receptors, TNF receptors, G-protein coupled receptors, methyl transferases, ligases, etc. The present sequence is the human PIM 1 protein. This sequence is used to illustrate the method of invention.
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20-SEP-2002;
02-JAN-2003;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Designing a ligand binding to a target molecule, comprises identifying molecular scaffolds compounds binding to members of a molecular family, detecting orientation of scaffolds at a binding site of target, and synthesizing ligand.
                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 313 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; SEQ ID NO 9; 186pp;
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                      EIHLHSLSPGPSK 313
                                                                               PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA
                                                                                                                      ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI
                                                                                                                                       ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI
                                                                                                                                                                                                   ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG
                                                                                                                                                                                                                                             NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL
 EIHLHSLSPGPSK 313
                                                                                                                                                                               ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG
                                                            PFEHDEETIRGOVFFRORVSSECQHLIRWCLALRPSDRPTFEETQNHPWMQDVLLPQETA
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                                                                                                                                                                                                                                                                                                                                                                100.0%;
ilarity 100.0%;
Conservative (
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; 2002US-0411398P.
; 2002US-0412341P.
; 2003US-0437929P.
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Pred. No. 1.4e-154;
); Mismatches 0;
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                                                                                                                                                                                                                                                                                  Query Match
Best Local (
                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                         hypersensitivity, urticaria, an immunologic disease of the lung, eosinophilic pneumonia, idiopathic pulmonary fibrosis, hypersensitivity pneumonitis, a transplantation associated disease, graft rejection or graft-versus-host disease. The present sequence represents a PRO protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         antiinflammatory, antiarthritic, antirheumatic, immunosupposteopathic, antidiabetic, dermatological antipsoriatic,
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renal disease, or demyelinating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New PRO polypeptides and polynucleotides, useful for treating e.g. erythematosus, rheumatoid arthritis, diabetes mellitus, immune-mediated renal disease, or demyelinating diseases of the central or peripheral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRO; antiinflammatory; antiarthritic; antirheumatic; immunosuppressive; osteopathic; antidiabetic; dermatological; antipsoriatic; antiallergic; antiasthmatic; hepatotropic; respiratory; gene therapy; immune system.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      polypeptide encoded by it. A protein of the invention has antiinflammatory, antiarthritic, antirheumatic, immunosuppressive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 7; SEQ ID NO 1405; 2940pp; English
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N-PSDB; ADP24226.
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                                                                                                                                                                                                                                                                                                                                                                Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            invention relates to a novel isolated nucleic acid and the PRO
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                                                                                                   19
                                                                                                                                                                                                                                                                                     Similarity
ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG
                                                                              NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL
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                                                NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL
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Pred. No. 1.4e-154;
; Mismatches 0;
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                                                                                                                                                                                                                                                                                                     Length 313;
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Matches 313;

Conservative

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Indels

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Query Match
Best Local (
                                                                                                                                             The invention relates to a method of screening a prophylactic-therapeutic agent for an apoptosis inducing agent or an enhancer of an anticancer agent. The method involves the use of a serine/threonine kinase Pim-1, its partial peptide or its salt. Also disclosed is a kit for carrying out the method of the invention. The method is useful for screening a prophylactic-therapeutic agent for cancer. The method is also useful for prophylaxis and/or treatment of cancer, inducing apoptosis, treating a patient having a solid tumour that is resistant to an anticancer agent (induced by hypoxia), and for screening a substance that promotes or inhibits the activity of serine/threonine kinase Pim-1. The present reguence represents a human polypeptide relating to the present
                                                                           Sequence 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Screening for a prophylactic-therapeutic apoptosis inducing agent or enhancer of anticancer agent, comprises use of serine/threonine kinase Pim-1, its partial peptide or its salt.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; SEQ ID NO 1; 93pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  03-APR-2003; 2003US-0459644P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human protein #1 associated to anticancer compound
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DB; ADT07366.
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100.0%;
Score 1670; DB 8;
Pred. No. 1.4e-154;
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Pim-1; cancer;
                        Length
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RESULT 12
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                Jacobs ML,
                                                  04-APR-2003; 2003US-0460843P
12-MAR-2004; 2004US-0552526P
                                                                           01-APR-2004; 2004WO-US010345
                                                                                                                                                       Modified-site
                                                                                                                                                                                                         Modified-site
                                                                                                                                                                                                                                                                                   Key
                                                                                                                                                                                                                                                                                                                     crystallography; Pim-1; cancer; serine/threonine kinase;
protein co-ordinate data; protein structure.
                                                                                                                                                                                                                                                                                                                                                                                               ADT14636 standard; protein; 313
WPI; 2004-757977/74
                                                                                                             WO2004090106-A2
                                                                                                                                                                                                                                          Domain
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                Hare B,
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/note= "OTHER = Forms a salt bridge via linkage to
Arg166"
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Crystal useful for developing Pim-1 (oncogene-encoded serine/threonine kinase) inhibitors, comprises human Pim-1 protein, Pim-1 homologue, human Pim-1 protein complex, or Pim-1 homologue complex.
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8 SEQ ID NO 2; 219pp; English.

The invention relates to a novel crystal comprising a human Pim-1 (Oncogene-encoded serine/threonine kinase) protein, a Pim-1 homologue, human Pim-1 protein complex or a Pim-1 homologue complex. Pim-1 is primarily expressed in haemopoietic and germ cell lines and this expression is tightly regulated and induced by cytokines, mitogens and hormones. Human Pim-1 is associated with multiple cellular functions, such as proliferation, differentiation, apoptosis and tumourigenesis. To crystal of the invention relates particularly to the residues involved the active site and binding sites of Pim-1. Such information may be useful for developing Pim-1 inhibitors that are useful as therapeutic agents in the treatment of cancer. The current sequence is that of the human Pim-1 (oncogene-encoded serine/threonine kinase) protein of the The in œ

Sequence 313 AA;

Length

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301
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EIHLHSLSPGPSK 313
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RESULT 13
ADY86782
ID ADY86
XX ADY86
XX ADY86
XX ADY86
XX P102-JU
XX Progr
KW Progr
KW Piml.
XX Piml.
XX US200
XX US200
XX YS200

Prognosis; Human 02-JUN-2005 ADY86782;

cancer; protein,

cytostatic; neoplasm; tyrosine threonine kinase;

TTK;

Pim1

SEQ ID NO:

18

(first entry)

Homo sapiens

27-SEP-2004; 2004US-00951477.

24-MAR-2005.

ADY86782 standard; protein; 313 AA

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RESULT 14
AEA89424
ID AEA89
XX
XX
AC AEA88
AC AEA88
XX
DT 25-AL
XX
DE Human
XX
KW Drug
KW Drug
KW Piml
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Best Local
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23-FEB-2001;
21-FEB-2002;
  Drug
Pim1
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                                  Human Piml
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           screening;
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)B; ADY86781.
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JEFFERSON
CHAN V W.
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                                                                                                     standard; protein;
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                                                                                                                                                                               EIHLHSLSPGPSK
                                                                                                                                                                                                            PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA
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                                 protein,
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2001US-0289813P.
2002US-00081119.
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            diagnosis;
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Pred. No. 1.4e-154;
Mismatches 0;
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           cancer;
           cytostatic;
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Matches 313
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21-FEB-2002;
06-FEB-2003;
30-OCT-2003;
22-JAN-2004;
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26-JUL-1999;
13-AUG-1999;
03-NOV-1999;
                                                                                                                                                                                                                                                                                                            The invention relates to human HX2004-6 protein and a seven transmembrane receptor protein referred as VSHK-1 useful for diagnosing or treating cancer. The invention also relates to a method for reducing the growth of a cancerous cell. VSHK-1 is useful for identifying a VSHK-1 receptor ligand and to identify a substance which modulates its signal transduction activity. The HX2004-6 DNA is useful to detect the presence of HX2004-6 in a biological sample (e.g. ductal epithelial cells from tissue chosen from pancreas, colon and breast). The invention is useful for screening drugs for the treatment of cancer. The present sequence is the human Piml protein. This sequence is differentially expressed in
                                                                                                                                                                                                                                                                             Sequence 313
                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; SEQ ID NO 18; 206pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated human HX2004-6 polypeptide o useful for diagnosing or treating cancer, identify a VSHK-1 receptor ligand.
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25-JUL-2000;
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PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA
                                                                                              ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG
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2000US-00570593.
2000US-00626301.
2001US-0271254P.
2002US-00061119.
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RESULT 15
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                                                                                                                                                                             Query Match
Best Local Similarity
Matches 313; Conserv
                                                                                                                                                                                                                                                                                      The invention relates to a novel method for identifying substances that regulate urinary incontinence and the urge to urinate. The method comprises incubating a test compound with a cell and/or cell preparation that has synthesized a specific protein of the PIM (proviral integration site) kinase family and measuring either binding of the test compound to the PIM kinase, or a functional parameter that is altered by the binding. The method of the invention demonstrates uropathic and gene therapy applications and may be useful for treatment and diagnosis of urinary incontinence and the urge to urinate. The method is based upon regulating the activity or expression of PIM kinases that are involved in bladder control. The current sequence is that of the human PIM-1 serine-threonine
                                                                                                                                                                                                                                             Sequence 313 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Identifying substances that regulate PIM kinases, useful for treatment and diagnosis of urinary incontinence and the urge to urinate, and similar use of PIM proteins or nucleic acids.
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N-PSDB; AEB96036.
REFSEQ; NP_002639.
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Search completed: May 4, 2006, 05:24:45 Job time : 118.667 secs

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376	υα	N N	S66730	hypothetical prote	A;Cross-rei R;Domen, J.
367	0 13	งผ	S33653	probable serine/th	Oncogene Re
361	<b>σ</b> (	N K	S52244	probable serine/th p69Eg3 protein - A	A;Title: Co A;Reference
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359	UT (	μ,	A56009	serine/threonine-s	A; Molecule
357 352	21.4 512 21.1 512	ผ ผ	T52633 T07788	serine/threonine-s probable serine/th	A;Residues: A:Cross-ref
348	о Ф	N	B90100		C; Comment:
347.5	<b>∞</b> α	N	B84644 T20941	<pre>probable protein k hypothetical prote</pre>	C;Genetics: A:Gene: GDE
345	7		T33998		A;Cross-ref
342.5	տ տ		T04862 T29253	probable serine/th	A;Map posit
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341 339.5	20.4 513		S60304 T07415	serine/threonine-s	A;Descripti C:Superfami
337	s N		T02306		C; Keywords:
. (	μ,	Ν1	T50802	serine/threonine p	F;44-52/Rec

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A; Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonin A; Note: in testis may be involved in signal transduction events of normal germ cell matu C; Superfamily: kinase-related transforming protein; protein kinase homology C; Keywords: ATP; autophosphorylation; phosphoprotein; phosphotransferase; proto-oncogene F; 36-290/Domain: protein kinase homology <KIN>F; 44-52/Region: protein kinase ATP-binding motif F; 67/Active site: Lys #status predicted
                                                                                                                                                                                                                                                                                                        A;Experimental source: testis
A;Note: testis-specific transcript is shorter
C;Comment: Pim-1 autophosphorylates at unknown
C;Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein kinase (EC 2.7.1.37) pim-1 - rat
N;Alternate names: kinase-related transforming
C;Species: Rattus norvegicus (Norway rat)
C;Date: 25-Feb-1994 #sequence_revision 21-Jan-1
C;Accession: S26298
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Nucleic Acids Res. 20, 3183-3189, 1192
A;Title: Characterization of the testes-specific pim-1 transcript
A;Reference number: S26298; MUID:92319652; PMID:1620615
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A; Residues: 1-313 <WIN>
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Pred. No. 9.2e-75;
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Pred. No. 1.9e-76;
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A;Cross-references: UNIPROT:P06803; UNIPARC:UPI00000294AF; GB:M13945; GB:M13946; NID:g20 C;Comment: Pim-1 autophosphorylates at unknown sites. C;Genetics:
A;Gene: pim-1
A;Introns: 28/1; 63/3; 80/3; 203/1; 262/1
C;Function:
C;Function: Catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonin C;Superfamily: kinase-related transforming protein; protein kinase homology C;Superfamily: kinase-related transforming protein; protein kinase homology C;Fuywords: ATF; autophosphorylation; phosphotransferase; proto-oncogene; serine/threonif;36-290/Domain: protein kinase homology KIN>
F;44-527/Region: protein kinase ATP-binding motif
F;67/Active site: Lys #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein kinase (BC 2.7.1.37) pim-1 - mouse
N;Alternate names: kinase-related transforming protein pim-1;
C;Species: Mus musculius (house mouse)
C;Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_chang
C;Accession: A24169
R;Selten, G; Cuypers, H.T.; Boelens, W.; Robanus-Maandag, E.;
Cell 46, 603-611, 1986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD
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PFEHDEETIKGQVFFRQTVSSECQHLIKWCLSLRPSDRPSFEETRNHPWMQGDLLPQAAS
                                 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA
                                                                                                                  EIKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI
                                                                                                                                                   ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI
                                                                                                                                                                                                                                 ERPEPVQDLFDFITERGALQEDLARGFFWQVLEAVRHCHNCGVLHRDIKDENILIDLSRG
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A,Map position: X
A,Start codon: CTG
A;Note: locus between A-raf and Act-7, near Kv4.1
A;Function:
C;Function:
C,Superfamily: kinase-related transforming protein; protein kinase homology
C,Superfamily: kinase-related transforming protein; protein kinase homology
C,Keywords: alternative initiators; ATP; autophosphorylation; phosphoprotein; phosphotra
F;89-345/Domain: protein kinase ATP-binding motif
              hypothetical protein F45H7.4 - Caenorhabditis elegans C;Speciaes: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #t C;Accession: T22255
R;Percy, C.
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A;Cross-references: UNIPARC:UPI00000278BF; GB:L41495;
A;Note: 34K form
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A;Residues: 'M',27-370 <VA2>
A;Cross references: UNIPARC:UPI00000278BE;
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A;Molecule type: mRNA
A;Residues: 'M',61-370
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   submitted to
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A; Residues: 1-370 < VAN>
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;Date: 10-Oct-1995 #sequence revision 21-Jan-1997 #text_change 09-Jul-2004
;Accession: S55333; A43093; B43093
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56.6%; Pred. No. 2.7e-37;
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A;Reference number: Z19538
A;Accession: T22255
A;Status: preliminary; translated from GE
A;Molecule type: DNA
A;Residues: 1-363 <WIL>
A;Cross-references: UNIPROT:Q20443; UNIPA
A;Experimental source: Clone F45H7
C;Genetics:
                                                                                                                                                                                                                                                                                    A; MOLECULE . 1-409 < FAV>
A; Residues: 1-409 < FAV>
A; Cross-references: UNIPARC: UPI000017B744;
A; Cross-references: strain Bristol N2
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A; Introns: 24/1;
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A;Introns: 72/3; 160/3; 310/1
C;Superfamily: protein kinase homology
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                                                                                                                                                                                                                                                                                                                                                                                                   submitted to the EMBL Data Library, February 1994 A; Description: The sequence of C. elegans cosmid C06E8
                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein C06E8.3 - Caenorha C;Species: Caenorhabditis elegans C;Date: 20-Sep-1999 #sequence_revision C;Accession: T15435
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Best Local S
Matches 120
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Matches 105;
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                                                                                                                                                    1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSG-IRVS
                                                                                                                                                                                                   Similarity
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                 LERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHN-CGVLHRDIKDENILIDLN 178
                                                                               DNLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLI
MERPANCMOLFOMVSVHGPLNEDMGKF1FKQV1TTVFNMYSKHGLLHRD1KDENLIVNMN
                                                          GQQPVAVKEVQHKHVRSW-TMTCRQLIPSEVCHL-ETCEDIPGVIKILDWFANSKGFLIV
                                                                                                                       MIKRKLODLAVCCSYQVDFLHEKK----HSVKEFKRKYEVLDEIGRGGFGIVYEATTROD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LTFDFFQRCSLEAILNHPWVKQQTL 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HSLYLGREAAVWSLGVLLYNSLNGRLPFRNEKDICTAHLLGPLPFFVPVSAEVKDLISKC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YHRYHGRSAAVWSLGILLYDMVCGDIPFEHDEEI----IRGQVFFRQRVSSECQHLIRWC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KVSSGFSGVIRLLDWFERPDSFVLILERPEPVQDLFDFITERGALQEELARSFFWQVLEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KKNYKLKAELGRGGFGVVYRAVRTCDNALVAVKFIERSNVKEWARI-NGEQVPMEICMLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ESQYQVGPLLGSGGFGSVYSGIRVSDNLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLK
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                                                                                                                                                                                                                                                E8.3
76/3;
                                                                                                                                                                                      Conservative
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                                                                                                                                                                                      55,
                                                                                                                                                                                   Score 486; DB 2;
Pred. No. 1.2e-17;
55; Mismatches 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 617;
Pred. No. 3.
                                                                                                                                                                                                                                                                                                                                                         from GB/EMBL/DDBJ
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.5e-24;
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RESULT 8
A;Cross-references: FlyBase:FBgn0000667
A;Introns: 205/3; 227/1; 322/3; 688/3;
A;Note: EG:22E5.8
                                                 A;Residues: 1-1398 <MUR>
A;Cross-references: UNIPROT:O77268; UNIPARC:UPI00000820A3; EMBL:AL031765; NID:e1371523;
C;Genetics:
                                                                                                                                                     C;Keywords: ATP
F;71-324/Domain: protein kinase homology <KIN>
F;79-87/Region: protein kinase ATP-binding motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mech. Dev. 48, 153-164, 1994
A;Title: Identification of novel protein kinases expressed A;Reference number: 149071; MUID:95200798; PMID:7893599
A;Accession: 149072
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein kinase - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Oct-2004
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                                                                                     A; Molecule type: DNA
A; Residues: 1-1398 <
                                                                                                                                       A; Reference number: A; Accession: T13741
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A;Molecule type: mRNA
A;Residues: 1-481 <RES>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R; Ruiz, J.C.; Conlon, F.L.; Robertson, E.J.
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Best Local S
Matches 99
                                                                                                                     Status: preliminary; translated
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DIPFEHDEEIIRGOVFFRORVSSECOHLIRWCLALRPSDRPTFEEIONHPWMQ 291
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                                                                                                                                                                                                                                                                                                                                                                LEGRFRIPFFMSQDCETLIRRMLVVDPAKRITIAQIRQHRWMQADPTLLQQD
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                 782/3; 814/2; 1363/3
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RESULT 9
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A;Map position: 15L
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A;Cross-references: UNIPROT:Q08217;
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A; Accession: $66730
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Date: 12-Jul-1996 #sequence_revision 12-Jul-1996 #text_change 05-Oct-2004 C;Accession: S66730
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein YOL045w - yeast (Saccharomyces cerevisiae) N;Alternate names: hypothetical protein O2034 C;Species: Saccharomyces cerevisiae
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 22.8%; Score 380; DB 2; Best Local Similarity 33.3%; Pred. No. 6.2e-12; Matches 92; Conservative 57; Mismatches 109
                                                                                                                                                                                                                                                                                                                                                                                             Matches
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Best Local Similarity
1074
                                                                           1014
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                                                                                                                                                                                                                                                                                                                                                                                             87;
                                                                                                                                                                            FFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRGELKLIDFGSGALLKDTVYTDFDGTRV 206
                                                                                                                                                                                                                                   ATLNKNSQENILKLLDFFEDDDYYYI----ETPVHGETGSIDLFDVIEFKKDMVEHBAKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDIPFEHD-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YREVEIMKRLK--HPHIIKLYQVMETKNMIYIVSEYASQ-GEIFDYIAKYGRMSESAARF
SLIKRILTREVDKRPTIDEIYEDKWLK 1100
                                    HLIRWCLALRPSDRPTFEEIQNHPWMQ 291
                                                                         YAAPEVLGGSSYKGKPQDIWALGVLLYTIIYKENPYYNIDEILEGELRFDKSEHVSEECI
                                                                                          YSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDIPFEHDEEIIRGQVFF--RQRVSSECQ 264
                                                                                                                                                   VFKQVVASIKHLHDQGIVHRDIKDENVIVD-SHGFVKLIDFGSAAXIKSGPFDVFVGTMD
                                                                                                                                                                                                                                                                        KKVS-SGFSGVIRLLDWFERPDSFVLILERPEPVQ-----DLFDFITERGALQEELARS 146
                                                                                                                                                                                                                                                                                                               SDFTILQVMGEGAYGKVNLCIHNREHYIVVIKMIFKERILVDTWVRDRKLGTIPSEIQIM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLL 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PYAAPEVFEGKOYTGPEIDIWSLGVVLYVLVCGALPFDGSTLQSLRDRVLSGRFRIPFFM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KFWQIISAVEYCHKKGIVHRDLKAENLLLDLNM-NIKIADFGFSNHFKPGELLATWCGSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRGELKLIDFG-SGALLKDTVYTDFDGTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLILERPEPVQDLFDFITERGALQEELARS 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KEKEPLE-SOYOVGPLLGSGGFGSV-YSGIRVSDNLPVAIKHVEKDRISDWGELPNGTRV
                                                                                                                                                                                                                                                                                                                                                  SQYQVGPLLGSGGFGSVYSGIRVSDNLPVAIKHVEKDRI--SDWGELPNGTRVPMEVVLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SSECEHLIRRMLVLEPTRRYTIDQIKRHRWMCPELL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KLKEPMRVGFYDIERTIGKGNFAVVKLARHRITKN-EVAIKIIDKSQL----DQTNLQKV
                                                                                                                                                                                                                                                                                                                                                                                        22.5%;
ilarity 32.6%;
Conservative 5
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                                                                                                                                                                                                                                                                                                                                                                                           Score 376; DB 2;
Pred. No. 8e-12;
9; Mismatches 105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              UNIPARC: UPI000012DF35; EMBL: Z74788;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          motif
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                                                                                                                                                                                                                                                                                                                                                                                             Indels
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                                                                               1073
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1339 RCVPKRPTIDDINNDKWL 1356

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A;Accession. ...
A;Molecule type: DNA
A;Residues: 1-72,'E',74-154 <SID>
A;Residues: 1-72,'E',74-154 <SID>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Molecule type: DNA
A;Residues: 1-1358 <CLA>
A;Residues: 1-1358 <CLA>
A;Cross-references: UNIPROT:P31374; UNIPARC:UPI000017A449; EMBL:L05146
A;Cross-references: UNIPROT:P31374; UNIPARC:UPI000017A449; EMBL:L05146
R;Ouellette, F.; Clark, M.W.; Keng, T.; Storms, R.K.; Zhong, W.; Zeng,
submitted to the EMBL Data Library, January 1993
A;Description: Sequencing of Chromosome I from Saccharomyces cerevisiae
A;Reference number: S36711
A;Accession: S36711
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C;Date: 30-Sep-1993 #sequence revision 02-Aug-1994 #text_change 05-Oct-2004
C;Date: 30-Sep-1993 #sequence revision 02-Aug-1994 #text_change 05-Oct-2004
C;Accession: S33653; S36717; S36732; JH0486
R;Clark, M.W.; Zhong, W.W.; Keng, T.; Storms, R.K.; Ouellette, B.F.F.; Barton, A.; Kalyesst 9, 543-549, 1993
Yeast 9, 543-549, 1993
A;Title: The YAL017 gene on the left arm of chromosome I of Saccharomyces cerevisiae
A;Reference number: S33653; MUID:93311122; PMID:8322517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Molecule type: DNA
A;Residues: 1-864,867-1358 <OUE>
A;Residues: 1-864,867-1358 <OUE>
A;Cross-references: UNIPARC:UPI0000052EA6; EMBL:L05146; NID:g171851; PIDN:AAC04940.1;
A;Cross-references: UNIPARC:UPI0000052EA6; EMBL:L05146; NID:g171851; PIDN:AAC04940.1;
R;Clark, M.W.; Zhong, W.W.; Keng, T.; Storms, R.K.; Barton, A.; Kaback, D.B.; Bussey, Yeast B, 133-145, 1992
A;Title: Identification of a Saccharomyces cerevisiae homolog of the SNF2 transcriptic A;Reference number: S22266; MUID:92221690; PMID:1561836
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Map position: 1L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Cross-references:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Gene: SGD: FUN31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Residues: 1-862 < CL2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Accession: S36732
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            probable serine/threonine protein kinase (EC 2.7.1.-) - yeast (Saccharomyces N;Alternate names: protein YAL002; protein YAL017w; secretory protein SSP138
                                                                                        1279
                                                                                                                                                                                                                                                                                                                                                                                                                                            1104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LGSGGFGSVYSGIRVSDNLPVAIKHVEKDRI--SDWGELPNGTRVPMEVVLLKKVS-SGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           site: Asp #status predicted
LRPSDRPTFEEIQNHPWM
                                                                                     GNPYEGOPODIWAIGILLYTVVFKENPFYNIDEILEGDLKFNNAEEVSEDCIELIKSILN
                                                                                                                                                                                                                                              VRHCHNCGVLHRDIKDENILIDLNRGELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIR
                                                                                                                                                                                                                                                                                                                     ENILRLLDFFEDDDYYYI----ETPVHGETGCIDLFDLIEFKTNMTEFEAKLIFKQVVAG
                                                                                                                                                                                                                                                                                                                                                                            SGVIRLLDWFERPDSFVLILERPEPVQ------DLFDFITERGALQEELARSFFWQVLEA 154
                                                                                                                                                                                                                                                                                                                                                                                                                                      MGEGAYGKVNLCIHKKNRYIVVIKMIFKERILVDTWVRDRKLGTIPSEIQIMATLNKKPH
                                                                                                                                                                                                   IKHLHDQGIVHRDIKDENVIVD-SKGFVKIIDFGSAAYVKSGPFDVFVGTIDYAAPEVLG
                                                                                                                    YHRYHGRSAAVWSLGILLYDMVCGDIPFEHDEEIIRGQVFFR--QRVSSECQHLIRWCLA 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22.0%; Score
33.7%; Pred.
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RESULT 12

$52244

$5996183 protein - African clawed frog C;Species: Xenopus laevis (African claw C;Date: 07-May-1995 #sequence_revision C;Accession: $52244
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A;Residues: 1-504 <GUM>
A;Cross-references: UNIPROT:P93113; UNIPARC:UPI00000A4B92; EMBL:Y10036
A;Cross-references: UNIPROT:P93113; UNIPARC:UPI00000A4B92; EMBL:Y10036
A;Cross-references: Cv. Masterpiece; cotyledon
C;Function:
C;Function:
A;Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threon
A;Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threon
C;Superfamily: SNF1-related protein kinase; protein kinase homology
C;Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase
F;6-260/Domain: protein kinase homology <KIN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              probable serine/threonine-specific protein kinase N;Alternate names: SNF1-related protein kinase C;Species: Cucumis sativus (cucumber) C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 C;Accession: T10449 R;Gumpel, N.J.
                                                                                                                                                                                                                                                                                      R;Roghi, C.; le Guellec, R.; Paris, J.; Couturier, A.; submitted to the EMBL Data Library, October 1992 A:Description: Eg3, selected by differential screening
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                                                                                                                                                         A;Cross-references: UNIPROT:Q91821; UNIPARC:UPI000017A463; EMBL:Z17205; NID:g609283;
                                                                                                                                                                                A; Molecule type: mRNA
A; Residues: 1-651 < ROG>
                                                                                                                                                                                                                         A; Status: preliminary
                                                                                                                                                                                                                                                A; Accession: S52244
                                                                                                                                                                                                                                                                 A;Description: Eg3, selected A;Reference number: S52243
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  Query Match
Best Local S
Matches 94
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Best Local S
Matches 90
                                                                                         ;19-27/Region:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CHRNMVVHRDLKPENLLLD-SKCNVKIADFGLSNIMRDGHFLKTSCGSPNYAAPEVISGK
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                                                                                         protein
                                                                                       protein kinase homology <l
protein kinase ATP-binding
                                                                                                                                                                                                                                                                                                                                                                                           African clawed frog
(African clawed frog)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
21.6%; Score 361; DB 2; 34.8%; Pred. No. 2.8e-11; tive 51; Mismatches 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21.9%;
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Pred. No. 1.3e-11;
1; Mismatches 105
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                                            Length 651;
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Similarity

Conservative

Indels

Gaps

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qik protein - chicken
N;Alternate names: Qin-induced kinase
C;Species: Gallus gallus (chicken)
C;Date: 17-Nov-2000 #sequence_revision 17-Nov-2000 #text_change 09-Jul-2004
C;Accession: JC7500
C;Accession: JC7500
                                                                              RESULT
JC1446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Xia, Y.; Zhang, Z.; Kruse, U.; Vogt, P.K.; Li, OBiochem. Biophys. Res. Commun. 276, 564-570, 2000 A;Title: The new serine-threonine kinase, Qlk, is
serine/threonine-specific protein kinase (BC 2.7.1.-)
N;Alternate names: protein kinase SNF1 homology
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #ta
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A; Contents: Embryo fibroblasts
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: mRNA
A; Residues: 1-798 < XIA>
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Best Local S
Matches 88
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                           CHNCGVLHRDIKDENILIDLNRGELKLIDFGSGALLKD-TVYTDFDGTRVYSPPEWIRYH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YQVGPLLGSGGFGSYYSGIRVSDNLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VSAVAYIHSQGYAHRDLKPENLLIDEDQ-NLKLIDFGLCAKPKGGL--DYHLMTCCGSPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LEAVRHCHNCGVLHRDIKDENILIDLNRGELKLIDFGSGALLKDTVYTDFD-----GTRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AMKNLS--HQHVCRLYHVIETPKKIFMVLEYC-PGGELFDYIIAKDRLTEEEARVFFRQI 118
                                                                                                                                                                                                                               EYEGPHLDIWSLGVVLYVLVCGSLPFDGPNLPTLRQRVLEGRFRIPYFMSEDCETLIRRM
                                                                                                                                                                                                                                                                    RYHGRSAAVWSLGILLYDMVCGDIPFEHD-----EEIIRGQVFFRQRVSSECQHLIRWC
                                                                                                                                                                                                                                                                                                        CHSHHIVHRDLKTENLLLDANM-NIKLADFGFGNFYKSGEPLSTWCGSPPYAAPEVFEGK
                                                                                                                                                                                                                                                                                                                                                                                                                   SGFSGVIRLLDWFERPDSFVLILERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LLKKVSSGFSGVIRLLDWFERPDSFVLILERPEPVQDLFDFITERGALQEELARSFFWQV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EELLKYYELHETVGTGGFAKVKLASHLITGEKVAIKIMDKESLGD--DLP---RVKTEID
                                                                                                                                                        LVVDPTKRITISQIKQHKWMQADPSLRQQ
                                                                                                                                                                                          LALRPSDRPTFEEIQNHPWMQ-DVLLPQE 298
                                                                                                                                                                                                                                                                                                                                                                                --HPHIIKLYQVMETKDMLYIVTEFAKN-GEMFDHLTSNGHLSESEARKKFWQILSAVEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                         YDIERTLGKGNFAVVKLARHRVTKTQVAIKIIDKTRL----DPSNLEKIYREVQIMKLLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YAAPELIQGKAYIGSEADIWSMGVLMYALMCGYLPFDDDNVMVLYKKIMRGKYEIPKWLS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 361; DB 2;
Pred. No. 3.4e-11;
0; Mismatches 115
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of serine/threonine kinases,
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                                                            Arabidopsis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           81
                 serine/threonine-specific protein kinase (EC 2.7.1.-) C;Species: Nicotiana tabacum (common tobacco) C;Date: 28-Apr-1995 #sequence_revision 28-Apr-1995 #te C;Accession: A56009 R;Muranaka, T.; Banno, H.; Machida, Y. Mol. Cell. Biol. 14, 2958-2965, 1994
                                                                                                                                     A56009
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Characterization

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A; Cross-references; UNIPARC:UPI000009DEE0; EMBL:X86966; NID:g928909; PIDN:CAA60529.1; PI R; Thuemmler, F; Kirchner, M; Teuber, R; Dittrich, P. Plant Mol. Biol. 29, 551-565, 1995
A; Title: Differential accumulation of the transcripts of 22 novel protein kinase genes in A; Reference number: S66314; MUID:96123233; PMID:8534852
A; Accession: S66334
A; Molecule type: DNA
A; M
                                                                                                                                                                                                                                                                                                                                    á
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: UNIPROT:Q38997; UNIPARC:UP1000012DE43; R;Thuemmler, F.; Kirchner, M.; Teuber, R.; Dittrich, P. submitted to the EMBL Data Library, May 1995 A;Description: Differential accumulation of the transcript;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: DNA
A; Residues: 1-512 < LEG>
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R;LeGuen, L.; Thomas, M.; Bianchi, M.; Halford, N.G.; Kreis, Gene 120, 249-254, 1992
A;Title: Structure and expression of a gene from Arabidopsis A;Reference number: JC1446; MUID:93013041; PMID:1339373
A;Accession: JC1446
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A;Accession: S58266
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Best Local :
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245
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RDLIPRMLVVDPMKRVTIPEIRQHPWFQ 272
                                                                    QHLIRWCLALRPSDRPTFEEIQNHPWMQ
                                                                                                                                                                                                                                                                                                                                        LEAVRHCHNCGVLHRDIKDENILIDLNRGELKLIDFGSGALLKDTVYTDFD-GTRVYSPP
                                                                                                                                                                                                                                                                                                                                                                                                                   ILRLFM--HPHITRLYEVIETPTDIYLVMEYVNS-GELFDYIVEKGRLQEDEARNFFQQI
                                                                                                                                        EVISGKLYAGPEVDVWSCGVILYALLCGTLPFD-DENIPNLFKKIKGGIYTLPSHLSPGA
                                                                                                                                                                                               EWIRYHRYHGRSAAVWSLGILLYDMVCGDIPFEHDEEI-----IRGQVF-FRQRVSSEC
                                                                                                                                                                                                                                                                          ISGVEYCHRNMVVHRDLKPENLLLD-SKCNVKIADFGLSNIMRDGHFLKTSCGSPNYAAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ESILPNYKLGRTLGIGSFGRVKIAEHALTGHKVAIKILNRRKIKN---MEMEEKVRREIK 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              51;
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Pred. No. 2.6e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                    291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      e from Arabidopsis
PMID:1339373
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C;Function:
A;Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonir A;Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonir A;Description: catalyzes the formation of protein kinase homology
C;Superfamily: SNF1-related protein kinase; protein kinase homology serine/threonine-specific protein kinase;
F;17-271/Domain: protein kinase homology <KIN>
F;25-33/Region: protein kinase ATP-binding mottf
F;48,671,42,144/Active site: Lys, Glu, Asp, Lys #status predicted
F;49,671,451/Binding site: magnesium (Asn, Asp) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tase of Saccharomyces cerevisiae.

A;Reference number: A56009; MUID:94217693; PMID:8164654

A;Recession: A56009

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-511 <MUR>

A;C;Function:

C;Function:
Search completed: May 4, 2006, 05:25:50 Job time : 22.3333 secs
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## **Protein Sequence Searches - February 2005**

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension .rup) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein. Archive database (UniPARC) at:

http://www.pir.uniprot.org/database/archive.shtml

If you have any questions regarding this information or your results, please contact any STIC searcher.

When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.

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Q8R2P0 MOUSE
PIM2 MOUSE
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Q7ZVJ BRARE
Q8F182 BRARE
Q6D152 BRARE
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**CC Le SUBUNIT: Binds to RP9 (By similarity).

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**CC Le SUBLARITY: Belongs to the Ser/Thr protein kinase family. PIM: Sachs T., Ryder J., Sachs T., Ryder J., PIM: Autophosphorylated on tyrosine residues.
EMBL; M27903; AAA60090.1; -; Genomic_DNA.
EMBL; M16750; AAA60089.1; -; mRNA.
EMBL; M24915; AAA36477.1; -; mRNA.
EMBL; M24779; AAA31553.1; -; mRNA.
EMBL; M24779; AAA81553.1; -; mRNA.
EMBL; BC020224; AAA70224.1; -; mRNA.
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the Euro
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Pasqualucci L., Neumeister P., Goossens T.,
Chaganti R.S.K., Kuppers R., Dalla-Favera R.
"Hypermutation of multiple proto-oncogenes i
cell lymphomas.";
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DATABASE:
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GO; GO:0004674; F:protein serine/threonine kinase activity; TAS.
GO; GO:0004775; P:development; TAS.
GO:0006468; P:protein amino acid phosphorylation; TAS.
InterPro; IPR000719; Prot kinase.
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PROSITE; PS00107; PROTEIN KINASE ATP; 1.
PROSITE; PS50011; PROTEIN KINASE DOM; 1.
PROSITE; PS00108; PROTEIN KINASE ST; 1.
3D-structure; ATP-binding; Kinase; Nuclear
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Ensembl; ENSG0000013719
HGNC; HGNC:8986; PIM1.
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2BIK; X-ray;
2BIL; X-ray;
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RESULT 3
PINI FELCA
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AC 095LJO;
DT 28-FEB-2003 (
DT 13-SEP-2005 (
DE Proto-oncoger
GN Name-PINI;
OS Felis silvest
OC Eukaryota; Me
OC Mammalia; Eut
OC Mammalia; Eut
OC MOBI_TAXID=96
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RP NUCLEOTIDE SE
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Best Local S
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SMART; SM00210; TYc; 1.

SMART; SM00219; TY-KC; 1.

SMART; SM00219; TY-KC; 1.

PROSITE; PS00107; PROTEIN KINASE ATP; 1.

PROSITE; PS00101; PROTEIN KINASE TY; 1.

PROSITE; PS00108; PROTEIN KINASE TY; 1.

ATP-binding; Kinase; Mucleotide-binding; Serine/threonine-protein kinase; Transferase.

SEQUENCE 313 AA; 35686 MW; 35BA76D3668E69A3
NUCLEOTIDE SEQUENCE. Fujino Y., Satoh H.,
                             NCBI_TaxID=9685;
                                            Eukaryota; Metazoa;
Mammalia; Eutheria;
Felinae; Felis.
                                                   Felis silvestris catus (Cat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Felidae;
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                                                                                              (Rel. 41, Created)
(Rel. 41, Last sequence update)
(Rel. 48, Last annotation update)
ene serine/threonine-protein kinase
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R SMR; Q95LJO; 32-308.

R InterPro; IPR00819; Prot kinase.

R InterPro; IPR008271; Ser_Thr_pkin_AS.

R Pfam; PF00069; Pkinase; 1.

R PfoBom; PD000001; Prot kinase; 1.

R ProDom; PD000001; Prot kinase; 1.

R PROSITE; PS00107; PROTEIN KINASE_ATP; 1.

R PROSITE; PS00118; PROTEIN_KINASE_DOM; 1.

R PROSITE; PS00108; PROTEIN_KINASE_TOM; 1.

R PROSITE; PS00108; PROTEIN_KINASE_TOM; 1.

R PROSITE; PS00108; PROTEIN_KINASE_TOM; 1.

W ATP-binding; Kinase; Nuclear protein; Nucleotide-binding; PROSED ATP PROSED ATP PROTEIN KINASE ATP PROTEIN KINASE ATP PROTEIN; PS00108; PROTEIN FINASE ATP PROTEIN; PS00108; PROTEIN FINASE ATP PROTEIN; PS00108; PROTEIN FINASE ATP PROTEIN; Nuclear PROTEIN; Nuclear Protein Kinase; Nucl
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-:- SUBCELLULAR LOCATION: Cytoplasmic and nuclear -:- PTM; Autophosphorylated (By similarity).
-:- SIMILARITY: Belongs to the Ser/Thr protein kin
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ATP (By similarity).
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Pred. No. 4.6e-114;
2; Mismatches 1;
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InterPro; IPR008271; Ser thr pkin AS.
Pfam; PP00069; Pkinase; I.
ProDom; PD000001; Prot kinase; 1.
PROSITE; PS00107; PROTEIN KINASE ATP; 1.
PROSITE; PS50011; PROTEIN KINASE DOW; 1.
PROSITE; PS00108; PROTEIN KINASE ST; 1.
PROSITE; PS00108; PROTEIN KINASE ST; 1.
ATP-binding; Kinase; Nuclear protein; Nucleotide-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIJINE-21109090; PubMed=11182156; DOI=10.1016/S0165-2427(00)00259-2; Wang Z., Petersen K., Weaver M.S., Magnuson N.S.; "CDNA Cloning, sequencing and characterization of bovine pim-1."; Vet. Immunol. Immunopathol. 78:177-195(2001).
-!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
-!- SUBCELLULAR LOCATION: Cytoplasmic and nuclear (By similarity).
-!- SUBCELLULAR LOCATION: Cytoplasmic and nuclear (By similarity).
-!- SIMCELLULAR LOCATION: Cytoplasmic and nuclear (By similarity).
-!- SIMILARITY: Belongs to the Ser/Thr protein kinase family. PIM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AF259078; AAF67200.1; -; mRNA.
HSSP; Q63450; 1A06.
SMR; Q9N0P9; 32-308.
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Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
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                                                                                             EIHLHSLSPGPSK 313
                                                                                                                                                                                                          ELKLIDFGSGALLKOTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI
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                                                                                                                                    PFEHDEEIVRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA
                                                                                                                                                   PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEEIQNHPWMQDVLLPQETA
                                                                                                                                                                                             ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI
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313 AA;
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ATP (By similarity).
Proton acceptor (By similarity)
ATP (By similarity).
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       PRT;
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodent
Muroidea; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it use as long as its content is in no way modified and this statement is no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=Sprague-Dawley; TISSUE=Testis; MEDLINE=92319652; PubMed=1620615;
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01-AUG-1992 (Rel.
13-SEP-2005 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ProDom; PD000001; Prot kinase; 1.

PROSITE; PS00107; PROTEIN KINASE ATP; 1.

PROSITE; PS00101; PROTEIN KINASE ST; 1.

PROSITE; PS00108; PROTEIN KINASE ST; 1.

ATP-binding; Kinase; Nuclear procein; Nucleotide-binding;

Phosphorylation; Proto-oncogene; Serine/threonine-protein kinase;
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InterPro; IPR000719; Prot kinase.
InterPro; IPR008271; Ser thr_pkin
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PIR; S26298; S26298.
SMR; P26794; 32-308.
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                                                                                                                                                                   ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG
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PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA
                                                                        ELKLIDFGSGALLKDTVYTDFDGTTVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI
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                                               ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI
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el. 23, Last sequence update)
el. 48, Last annotation update)
serine/threonine-protein kinase
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ATP (By similarity).
Proton acceptor (By s
ATP (By similarity).
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Pred. No. 2.3e-112;
6; Mismatches 3;
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RC STRAINCSTBL/6; TISSUB=Brain, and Eye;

RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausmer R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Hillon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

RA Hillalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Hillalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Generation and initial analysis of more than 15,000 full-length human

RT and mouse cDNA sequences.";

Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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                                                                                                                                                                                    Strausberg R.;
Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosph
-!- SIMILARITY: Belongs to the Ser/Thr protein kinase far
EMBL; BC042885; AAH42885.1; -; mRNA.
EMBL; BC053019; AAH53019.1; -; mRNA.
EMBL; BC055316; AAH55316.1; -; mRNA.
SMR; QSCFNB; 32-308.
Ensembl; ENSMUSG00000024014; Mus musculus. MGI; MGI:97584; Piml. GO; GO:0005524; F:ATP binding; IEA. GO; GO:0004674; F:protein serine/threonine GO; GO:0004678; P:protein amino acid phosph InterPro; IPR000719; Prot_kinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=C57BL/6; TISSUE=Brain; Strausberg R.; Submitted (JUN-2003) to the E
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10-MAX-2003 (TrEMBLrel. 23, Last sequence update)
10-MAX-2005 (TrEMBLrel. 30, Last annotation update)
Proviral integration site 1.
Name=Piml;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Strausberg
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Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia, Sciurognathi,
Muridae, Murinae, Mus.
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Best Local :
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InterPro; IPR002290; Ser_thr_pkinase.
Pfam; PP00069; Pkinase; 1.
ProDom; PD000001; Prot_kinase; 1.
SWART; SM00220; S_TKG; 1.
SWART; SM00220; S_TKG; 1.
PROSITE; PS00107; PROTEIN_KINASE_DOM; 1.
PROSITE; PS00108; PROTEIN_KINASE_DOM; 1.
PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
PROSITE; PROTEIN_KINASE_ST; 1.
PROSITE; PROTEIN_KINASE_ST; 1.
PROSITE; PROTEIN_KINASE_ST; 1.
PROSITE; PROTEIN_KINASE_ST; 1.
PROSITE PROTEIN_KINASE_ST; 1.
PROSITE PROTEIN_KINAS
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INTERACTION WITH RP9.

MEDLINE=20389540; PubMed=10931201;

Maita H., Harada Y., Nagakubo D., Kitaura H., Ikeda

Maita H., Harada Y., Nagakubo D., Kitaura H., Ikeda

Takahashi K., Ariga H., Iguchi-Ariga S.M.M.;

"PAP-1, a novel target protein of phosphorylation by

Eur. J. Biochem. 267;5168-5178(2000).

-i- CATALYTIC ACTIVITY: ATF + a protein = ADF + a ph

-i- SUBCELLULAR LOCATION: Cytoplasmic and nuclear (B
                                                                                                                                                                                                                Selten G., Cuypers H.T., Boelens W., Robomen J., van Beveren C., Berns A., "The primary structure of the putative homology with protein kinases."; Cell 46:603-611(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JAN-1988 (Rel. 06, Created)
01-JAN-1988 (Rel. 06, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
Proto-oncogene serine/threonine-protein kinase
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MEDLINE=86272109; PubMed=3015420;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Name=Pim1; Synonyms=Pim-1; Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                   Muroidea;
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Muridae; M
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Chordata; Craniata; Vertel
Euarchontoglires; Glires;
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                                                                                                                                                                                                                                                                                                        DOI=10.1016/0092-8674(86)90886-X;
W., Robanus-Maandag E., Verbeek J.
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No. 9.
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                                             phosphoprotein.
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    similarity)
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RESULT 8
PIM3_COTJA

ID PIM3_COTJA STANDARD; PRT; 323

AC Q9PUB5;
DT 28.FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence updated)
DT 13-SEP-2005 (Rel. 48, Last annotation updated)
DT 13-SEP-2005 (Rel. 48, Last annotation updated)
DE Serine/threonine-protein kinase Pim-3 (B)

Name=PIM3; Synonyms=PIM-3;
OS Coturnix coturnix japonica (Japanese qua
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Best Local S
Matches 294
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ACT SITE
BINDING
SEQUENCE
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InterPro; IPR00871; Ser_thr_pkin_AS.
Pfam; PF00069; Pkinase; 1.
ProDom; PD000001; Prot_kinase; 1.
PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS00101; PROTEIN_KINASE_Tom; 1.
PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
ATP-binding; Kinase; Nuclear protein; Nucleotide-binding;
ATP-binding; Kinase; Nuclear protein; Nucleotide-binding;
ATP-binding; Kinase; Nuclear protein; Nucleotide-binding;
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PIR; A24169; TVMSP1.
HSSP; Q63450; 1A06.
SMR; P06803; 32-308.
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DISEASE: Frequently activated by provirus insertion in mur
leukemia virus-induced T-cell lymphomas.
SIMILARITY: Belongs to the Ser/Thr protein kinase family.
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  (Japanese quail)
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Pred. No. 2.2e
10; Mismatches
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ATP (By similarity).
Proton acceptor (By similarity)
ATP (By similarity).
79F4779E9DCBDC16 CRC64;
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(EC 2.7.
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Matches 209
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-i- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprote:
-i- PTM: Autophosphorylated.
-i- SIMILARITY: Belongs to the Ser/Thr protein kinase family. I
                                                                                                                                                                                                                                                                                                                                             NP BIND
ACT SITE
BINDING
SEQUENCE
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SMART; SM00220; S. TKG; 1.

PROSITE; PS00107; PROTEIN KINASE_ATP; 1.

PROSITE; PS50011; PROTEIN KINASE_DOM; 1.

PROSITE; PS00108; PROTEIN_KINASE_ST; 1.

ATP-binding; Kinase; Nucleotide-binding; Phosphorylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This Swiss-Prot entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restruce as long as its content is in no way modified and this s
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Coturnix.
NCBI_TaxID=93934;
                                                                                                                                                                                                                                                                                                                                                                                             Serine/threonine-protein kinase; Transferase.
DOMAIN 40 291 Protein kinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AJ130845; CAB62386.1; -; HSSP; Q63450; 1A06.
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Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasiani
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                [nterPro;
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300
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Pro; IPR008271; Ser thr pkin AS.
Pro; IPR002290; Ser thr pkinase.
PF00069; Pkinase; I.
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                                                                                                                                                                                                             SDNLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVL
                                                                                                                                                                                                                                               MLLSKFGSLAHICSPASMDHLPVKILPPVKVEKEPFDKVÝQVGSVLGSGGFGTVÝAGSRT
EDCDIRLRTL
                       ETAEIHLHSL
                                                                                                                                               VMERPELVKDLFDFTTEKGALDEDTARGFFRQVLEAVRHCYGCGVVHRDTKDENLLVDLR
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ATP (By similarity).
Proton acceptor (By similarity).
ATP (By similarity).
; E2A4FA20B6F6396C CRC64;
                                                                                                                                                                                                                                                                                                          Score 1140; DB Pred. No. 8e-76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mRNA.
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RESULT 9
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ID PIM3\_HUMAN

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RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Carpleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Butterfield Y.S.N., Krzywinski M.I., Scheutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RA "Generation and initial analysis of more than 15,000 full-length human RT and mouse cDNA sequences.";
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                            This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chichester C., Nikitin F., Ravarini J.-C., Lisacek F.;
"Consistency checks for characterizing protein forms.";
Comput. Biol. Chem. 27:29-35(2003).
-i- FUNCTION: May be involved in cell cycle progression and appropriate process. Implicated in proliferation of human
                                                                                                                    EMBL; AB114795; BAD42438.1; -; EMBL; BC052239; -; NOT ANNOTATE Ensembl; ENSG00000198355; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Aberrant expression of serine/threonine hepatocellular carcinoma development and of human hepatoma cell lines.":
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 O86V86; (Nobell, 29-MAR-2004 (Rel. 43, Created)
29-MAR-2004 (Rel. 43, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
13-SEP-2005 (Rel. 48, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=22682943; PubMed=12798037; DOI=10.1016/S1476-9271(02)00095-6; Chichester C., Nikitin F., Ravarini J.-C., Lisacek F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=22388257; PubMed=12477932;
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Kaneko S., Mukaida N.
                                                                                 HGNC; HGNC:19310; PIM3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Liver
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Cell lines.

CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprot TISSUE SPECIFICITY: Widely expressed. No expression in company the state of the series of the series
                                                                                                                                                                                                                                                                                                                                                                      s Swiss-Prot entry is copyright. It is produced ween the Swiss Institute of Bioinformatics and European Bioinformatics Institute. There are r
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    IPR000719;
IPR008271;
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Euarchontoglires; Primates;
Prot_kinase.
Ser_thr_pkin_AS
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RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].

RC STRAIN=FVB/N; TISSUE-Colon, and Salivary gland;

RX MEDLINE=22388257; PubMed=12477912; DOI=10.1073/pnas.242603899;

RX MEDLINE=22388257; PubMed=12477912; DOI=10.1073/pnas.242603899;

RX MEDLINE=2388257; PubMed=12477912; DOI=10.1073/pnas.242603899;

RX MEDLINE=2388257; PubMed=16.10.1073/pnas.242603899;

RX MEDLINE=2388257; PubMed=10.1073/pnas.242603899;

RX MEDLINE=2388257; PubMed=10.1073/pnas.242603899;

RX MEDLINE=2388257; PubMed=10.1073/pnas.242603899;

RX MEDLINE=2388257; PubMed=10.1073/pnas.242603899;

RA Klausner R.D., Collins F.S., Wagner L.M., Schuelr G.D., Mat S.T., Wang J., Hsieh F.,

RA Alpins R.F., Jordah H., Moore T., Max S.I., Wang J., Hong L.,

RA Diacchenko L., Marusina K., Farmer A.A., Rabin G.M., Hong L.,

RA Stapleton M.J., Usdin T.B., Bonaldo M.F., Casavant T.L., Schuetz T.E.,

RA Brownstein M.J., Usdin T.B., Bonaldo M.F., Casavant T.L., Schuetz T.E.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Morley K.C., Hale S., Garcia A.M.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Willalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Willalon D.K., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
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ProDom; PD00001; Prot KINASE_ATP; 1.

PROSITE; PS00107; PROTEIN KINASE_DOM; 1.

PROSITE; PS00108; PROTEIN_KINASE_T; 1.

PROSITE; PS00108; PROTEIN_KINASE_ST; 1.

ATP-binding; Kinase; Nucleotide-binding; Phosphorylation;

ATP-binding; Kinase; Nucleotide-Transferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniat.
Mammalia; Eutheria; Euarchontoglires;
Muroidea; Murinae; Mus
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ACT SITE
BINDING
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Pred. No. 2
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oglires; Glires; Rodentia; Sciurognathi;
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RESULT 11
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Matches 213
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R InterPro; IPR000719; Prot kinase.

R InterPro; IPR008271; Ser_thr_pkinase.

R InterPro; IPR008271; Ser_thr_pkinase.

R InterPro; IPR008290; Ser_thr_pkinase.

R Pfam; PF00069; Pkinase; 1.

R ProDom; PD000001; Prot_kinase; 1.

R PROSITE; SM00220; S_TKC; 1.

R PROSITE; PS00107; PROTEIN KINASE DOM; 1.

R PROSITE; PS00108; PROTEIN KINASE T; 1.

R PROSITE; PS00108; PROTEIN KINASE DOM; 1.

R PROSITE; PS00107; PROTEIN KINASE DOM; 1.

R PROSITE; PS00107; PROTEIN KINASE DOM; 1.

R PROSITE; PS00107; PROTEIN KINASE DOM; 1.

R PROSITE; PS00108; PROTEIN KINASE DOM; 1.

R P
PIM3 RAT STANDARD; PRT; 326 AA.
070444;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
Serine/threonine-protein kinase Pim-3 (EC 2.7.1.37)
Kid-1) (Kinase induced by depolarization).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length and mouse cDNA sequences.", Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

-!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
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EMBL; BC026639; AAH26639.1; -; mRNA.
HSSP; Q03565; 1HOW.
Ensembl; ENSMUSG00000035828; Mus musculus.
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ATP (By similarity).
Proton acceptor (By similarity)
ATP (By similarity).
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Pred. No. 4.8e
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-!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
-!- TISSUE SPECIFICITY: Present in a number of unstimulated tissues of the state of 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Probom; PD000001; Prot_ kinase; 1.

SMART; SM00220; S_TKC; 1.

PROSITE; PS00101; PROTEIN_KINASE_DOM; 1.

PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.

PROSITE; PS00108; PROTEIN_KINASE_DOM; 1.

PROSITE; PS00108; PROTEIN_KINASE_DOM; 1.

ATP-binding; Kinase; Nucleotide-binding; Phosphorylation; Sering/threonine-protein kinase; Transferase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GO; GO:0004674; F:protein serine/threonine GO; GO:0046777; P:autophosphorylation; IDA. GO; GO:004572; P:histone phosphorylation; InterPro; IPR000719; Prot_kinase. InterPro; IPR008271; Ser_thr_pkinase. Pfam; PF00069; Pkinase; T.
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EMBL; AF057026; AAC36065.1;
HSSP; Q03656; 1HOW.
RGD; 620462; Pim3.
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Konietzko U., Kuhl D.;
"Pim-3 is a member of the pim kinase family.";
submitted (AUG-1998) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rattus norveĝicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
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INDUCTION: By membrane depolarization or forskolin.
PTM: Autophosphorylated.
SIMILARITY: Belongs to the Ser/Thr protein kinase f
subfamily.
119
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                                    FVLILERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILI
   FLLVLERPEPAQDLFDFITERGALDEPLARRFFAQVLAAVRHCHNCGVVHRDIKDENLLV
                                                                                                                                                                                                                                           MLLSKFGSLAHL-CGPGGVDHLPVKILQPAKADXESFEKVYQVGAVLGSGGFGTVYAGSR
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-; mRNA.
                                                                                                                                                                                                                                                                                                                                                                             Score 1128.5;
Pred. No. 5.7e
31; Mismatches
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ATP (By similarity).
Proton acceptor (By similarity)
ATP (By similarity).
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Length
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PRESULT TO THE PROPERTY OF SOLUTION OF SOL
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RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Richards S., McTley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakseley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT and mouse CDNA sequences.",
RI Proc. Narl Acad Sci U.S. A 90.16890-15901(2002)
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  Query Match
Best Local S
Matches 213
                                                                                                                                  Pfam; pF00069; pkinase; 1.

ProDom; pD000001; prot_kinase; 1.

SMART; SM00220; S_TKC; 1.

SWART; SM00220; TyrKC; 1.

PROSITE; pS00107; PROTEIN_KINASE_ATP; 1.

PROSITE; pS00107; PROTEIN_KINASE_DOM; 1.

PROSITE; PS00108; PROTEIN_KINASE_ST; 1.

ATP-binding; Hypothetical_protein; Kinase; Nucleotide-binding;

Serine/threonine-protein kinase; Transferase.

NON_TER

1 1
                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (JUN-2005) to the EMBL/GenB
-!- SIMILARITY: Belongs to the Ser/Th
EMBL; BC097317, AAH97317.1; -; mRNA.
InterPro; IPR000719; Prot_kinase.
InterPro; IPR0008271; Ser_thr_pkin_AS.
InterPro; IPR008271; Ser_thr_pkinase.
InterPro; IPR001245; Tyr_pkinase.
InterPro; IPR001245; Tyr_pkinase.
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Q4V8M2;
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Eukaryota; Metazoa; Chordata; Craniata;
Mammalia; Eutheria; Euarchontoglires; Gi
Muroidea; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NIH MGC Project;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Placenta;
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13-SEP-2005 (TrEMBLrel. 31, Last
13-SEP-2005 (TrEMBLrel. 31, Last
Hypothetical protein (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUCLEOTIDE SEQUENCE.
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                            Similarity
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                                                                                                              41568 MW;
                            67.6%;
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the Ser/Thr protein
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                            Score 1128.5;
Pred. No. 6.8
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                                                                                                              F82BE8E50DD71346
Mismatches
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annotation update)
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lires; Rodentia; Sciurogna
                            8e-1
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                                                    DB 2;
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n kinase family.
                                                                                                              CRC64;
  Indels
                                                       Length 380;
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7;
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Best Local
Matches 21
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01-JUN-2003
01-JUN-2003
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Muridae; Murinae;
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus
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                       116
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                                                                                 60
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212; Conser
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SMR; Q811X8; 30-22...

MGI; MGI:1355297; Pim3.

GO; GO:0005524; F:ATP binding; IEA.

GO; GO:000524; F:Protein serine/threonine kinase activity; IEA.

GO; GO:0004674; F:protein amino acid phosphorylation; IEA.

InterPro; IPR000719; Prot kinase.

R InterPro; IPR008271; Ser thr_pkin_AS.

R Pfam; PF00069; Pkinase; I.

PR PROSITE; PS00107; PROTEIN KINASE ATP; 1.

DR PROSITE; PS00107; PROTEIN KINASE TOM; 1.

DR PROSITE; PS00101; PROTEIN KINASE TOM; 1.

DR PROSITE; PS00101; PROTEIN KINASE TOM; 1.

DR PROSITE; PS00108; PROTEIN KINASE TT; 1.

KW ATP-binding; Kinase; Nucleotide-binding;

KW Serine/threonine-protein kinase; Transferase.

KW Serine/threonine-protein kinase; Transferase.

SCOUENCE 325 AA; 35931 MW; 77DEF8E20F41E3F4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (JAN-2001) to the EMBL/GenBank/DDBJ-!- SIMILARITY: Belongs to the Ser/Thr proteir EMBL; AY026239; AAK16606.1; -; mRNA. HSSP; Q03656; 1Q99.
SMR; Q811X8; 36-292.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Name=Pim3; Synonyms=Kid1;
119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MLLSKINSLAHLRAAP--CNDLHATKLAPGK-EKEPLESQYQVGPLLGSGGFGSVYSGIR
VSDNLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKV--SSGFSGVIRLLDWFERPDS
                                                                                                                                                                       MLLSKINSLAHLRAAP--CNDLHATKLAPGK-EKEPLESQYQVGPLLGSGGFGSVYSGIR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MLLSKFGSLAHL-CGPGGVDHLPVKILQPAKADKESFEKVYQVGAVLGSGGFGTVYAGSR
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                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                          66.8%;
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2; Mismatches
                                                                                                                                                                                                                                            Score 1116;
Pred. No. 4.
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XENLA
                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                               ProDom; PD000001; Prot_kinase; 1.
PROSITE; PS00107; PROTEIN KINASE_ATP; FALSE_NEG.
PROSITE; PS50011; PROTEIN_KINASE_DOW; 1.
PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
ATP-binding; Kinase; Nucleotide-binding; Phosphorylation;
Serine/threonine-protein kinase; Transferase.
                                                                                                                                                                                                                                                                                                                                                                  EMBL; L29495; AAA85389.1; -; mRNA
InterPro; IPR000719; Prot kinase.
InterPro; IPR008271; Ser_thr_pkin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Aebersold R., Pelech S.L.;
"Identification of the autophosphorylation sites of the Xenopu "Identification of the autophosphorylation sites of the Xenopu Pim-1 proto-oncogene-encoded protein kinase.";
J. Biol. Chem. 272:10514-10521(1997).
-!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprote
-!- PTM: Autophosphorylated.
-!- STMILARITY: Belongs to the Ser/Thr protein kinase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUCLEOTIDE SEQUENCE, AND PHOSPHORYLATION SITES.
MEDLINE=97256766; PubMed=9099695; DOI=10.1074/jbc.272.16.10514;
Palaty C.K., Kalmar G., Tai G., Oh S., Amankawa L., Affolter M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Cranīata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Xenopus; Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Name=PIM3; Synonyms=PIM1;
Xenopus laevis (African clawed frog)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
Serine/threonine-protein kinase Pim-3 (EC 2.7.1.37)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       subfamily. (Ref.1) called Pim-1 but seems
                                                                                                                                                                                                                                                                                                                                                                                                                                                        European
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               represent the pim-3 isoform.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        XENLA
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                                                                      Similarity
                     MLLSKINSLAHLRAAPCN-----DLHATKLAPGK-EKEPLESQYQVGPLLGSGGFGSVYS
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 MLLSKFGSLAHI - - - -
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69
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                                                                                                                 36964 MW;
                                                                      66.2%;
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 CNPSNMEHLPVKILQPVKVDKEPFEKVYQVGSVVASGGFGTVYS
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                                                          47;
                                                        Score 1105; Di
Pred. No. 3e-7.
47; Mismatches
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Phosphoserine (by autocatalysis)
Phosphothreonine (by autocatalys
                                                                                                                                                                                     Proton acceptor (By similarity).
ATP (By similarity).
Phosphoserine (by autocatalysis)
                                                                                                                                                                                                                                   Protein kinase.
ATP (By similarity)
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                                                        e 1105; DB 1;
. No. 3e-73;
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                                                                                    Length 323;
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ID Q66111;
AC Q6611;
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RA Altschul S.F., Zeebbrg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Zeebbrg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Stapleton M.J., Wadin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Stapleton M.J., Wadin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Rodrigues S., Sanchez A.,
RA Hakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Schnerch A., Schein J.E., Jones S.J.M., Narra M.A.;
RGeneration and initial snalvate of more than 15 non full length human
                                                                                                                             Q66II1_XENTR PRELIMINARY;
Ensembl; ENSXETG00000009354; Xenopus tropicalis. GO; GO:0005524; F:ATP binding; IEA. GO:0004674; F:protein serine/threonine kinase activity; GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                    "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences."; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Embryo;
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Xenopus tropicalis (Western clawed frog) (Silurana tropicalis).
Eukaryota; Metazoa; Chordata; Craniata; Verrebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus; Silurana.
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Search completed: May 4,
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InterPro; IPR008711; Ser_thr_pkinase.

BR InterPro; IPR008291; Ser_thr_pkinase.

BR InterPro; IPR008290; Ser_thr_pkinase.

BR InterPro; IPR001245; Tyr_pkinase.

BR InterPro; IPR001245; Tyr_pkinase.

BR Fam; PF00069; Pkinase; 1.

BR ProDom; PD000001; Prot kinase; 1.

BR SMART; SM00220; S_TKC; 1.

BR SMART; SM00220; S_TKC; 1.

BR SMART; SM00220; S_TKC; 1.

BR RROSITE; PS00107; PROTEIN KINASE_DOM; 1.

BR PROSITE; PS00101; PROTEIN KINASE_ST; 1.

BR PROSITE; PS00101; PROTEIN KINASE_ST; 1.

BR PROSITE; PS00108; PROTEIN KINASE_ST; 1.

BR PROSITE; PS00108; PROTEIN KINASE_ST; 1.

BR RROSITE; PS00108; PROTEIN KINASE; Nucleotide-binding; SEQUENCE 318 AA; 36547 MW; 48CCF12797F01FDC CRC64;
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## ALIGNMENTS

US-09-237-543-8 RESULT 1

Sequence 8, Application US/09237543A

Parent No. 6143540

GENERAL INFORMATION:
APPLICANT: Kapeller, Rosana
ITILE OF INVENTION: NOVEL MOLECULES OF THE HK
ITILE OF INVENTION: AND USES THEREOF
FILE REFERENCE: 035800/175631

CURRENT APPLICATION UNMBER: US/09/237,543A

CURRENT FILING DATE: 1999-01-26

NUMBER OF SEQ ID NOS: 11

SOPTWARE: Patentin Ver. 2.0

SEQ ID NO 8

LENGTH: 313

HKID-1-RELATED PROTEIN FAMILY

; TYPE: PRT ; ORGANISM: Rattus US-09-237-543-8

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Length 313;

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RESULT 2 US-09-644-450-8

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Sequence 9, Application US/09237543A

Patent No. 6143540

GENERAL INFORMATION:
APPLICANT: Kapeller, Rosana

ITILE OF INVENTION: NOVEL MOLECULES OF THE HKID-1-RELATED PROTEIN FAMILY
ITILE OF INVENTION: AND USES THEREOF

FILE REFERENCE: 035800/175631

CURRENT APPLICATION NUMBER: US/09/237,543A

CURRENT APPLICATION NUMBER: US/09/237,543A

CURRENT FILING DATE: 1999-01-26

NUMBER OF SEQ ID NOS: 11

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 9

LENGTH: 313

TYPE: PRT

ORGANISM: Homo sapiens
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TITLE OF INVENTION: NOVEL MOLECULES OF THE HK:
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: 035800/175631
CURRENT APPLICATION NUMBER: US/09/644,450
CURRENT FILING DATE: 2000-08-23
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 8
LENGTH: 313
TYPE: PRT
ORGANIAN: Rattus norvegicus
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                                                                    Score 1636; DB 2;
Pred. No. 3e-161;
6; Mismatches 3;
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GENERAL INFORMATION:
APPLICANT: Kapeller, Rosana
ITITLE OF INVENTION: NOVEL MOLECULES OF THE
ITITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: 035800/175631
CURRENT APPLICATION NUMBER: US/09/644,450
CURRENT FILING DATE: 2000-08-23
NUMBER OF SEQ ID NOS: 11
SOFTWARE: Patentin Ver: 2.0
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LENGTH: 313
TYPE: PRT
ORGANISM: Homo
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Best Local Similarity 97.1%;
Matches 304; Conservative
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                                                                  PFEHDEEIVKGQVYFRQRVSSECQHLIRWCLSLRPSDRPSFEEIQNHPWMQDVLLPQATA 300
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 EIHLHSLSPGPSK
                        EIHLHSLSPSPSK 313
                                                    PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA
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Pred. No. 3e-161;
6; Mismatches
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
SOFTWARE: Petentin #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,081B
FILING DATE: 5-UN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/104,736
FILING DATE: 10-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/796,066
FILING DATE: 10-NOV-91
ATTORNEY/AGENT INFORMATION:
APPLICATION NUMBER: D66
REFERENCE/DOCKET NUMBER: P66
REFERENCE/DOCKET NUMBER: P66
TELECOMMUNICATION INFORMATION:
TELEPAX: (213) 622-7700
TELEFAX: (213) 639-4210
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (213) 489-4210 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 313 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Smith, Kendall A. & Beadling, Carol
TITLE OF INVENTION: Nucleic Acids Encoding CR5 Polypeptide,
TITLE OF INVENTION: Vector and Transformed Cell Thereof, and Expression
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: PRETTY, SCHROEDER & POPLAWSKI
STREET: 444 South Flower St. - Suite 1900
CITY: Los Angeles
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
                                                            301
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                                               EIHLHSLSPSPSK 313
                                                                                                         PFEHDEEIVKGQVYFRQRVSSECQHLIRWCLSLRPSDRPSFEEIQNHPWMQDVLLPQATA 300
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                              EIHLHSLSPGPSK 313
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                                                                                          PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA
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Pred. No. 6.7e-160;
6; Mismatches 5;
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TYPE: peptide
; STRANDENNESS: n
; TOPOLOGY: n.a.
; MOLECULE TYPE: pe
US-08-461-379A-26
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Best Local S
Matches 302
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APPLICANT: Smith, Ken
TITLE OF INVENTION: N
TITLE OF INVENTION: E
TITLE OF INVENTION: E
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Rather & Prestia
ADDRESSEE: (B) STREET:One Westlakes-Berwyn
CITY: Valley Forge
STATE: Penneylvania
COUNTRY: USA
ZIP: 19482
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMpatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Petentin Release #1.0,
SOFTWARE: Petentin Release #1.0,
SOFTWARE: Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461,379A
FILING DATE: 5-JUNE-1995
PRIOR APPLICATION NUMBER: US/08/330,108; 08/104,736
APPLICATION NUMBER: US/08/330,108; 08/104,736
APPLICATION NUMBER: 07/796,066
FILING DATE: 27-OCT-1994; 10-AUG-1993 & 20-NOV-91
ATTORNEY/AGENT INFORMATION
NAME: Viviana Amzel, Ph. D.
REGISTRATION NUMBER: 30,930
DESEPRENCE/COUNTER NUMBER: 30,930
DESEPRENCE/COUNTER NUMBER: 30,930
DESEPRENCE/COUNTER NUMBER: 30,930
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INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 313 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: DA
TELECOMMUNICATION INFORMATION:
TELEPHONE: (610)470-0700
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302; Conserv
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5871961
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EIHLHSLSPSPSK 313
                                                       PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWWQDVLLPQETA
                                                                          PFEHDEEIVKGQVYFRQRVSSECQHLIRWCLSLRPSDRPSFEEIQNHPWMQDVLLPQATA
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Nucleic Acids Encoding CR5 Polypeptide,
Vector and Transformed Cell Thereof, and
Expression Thereof
S: 35
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PALLICATION DATA:
APPLICATION NUMBER: US/08/462,390B
FILING DATE: 5-JUNE-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USN 08/330,108
FILING DATE: 27-OCT-1994
APPLICATION NUMBER: USN 08/104,736
FILING DATE: 10-ANG-1993
APPLICATION NUMBER: USN 07/796,066
FILING DATE: 20-ANG-1993
APPLICATION NUMBER: USN 07/796,066
FILING DATE: 20-ANG-1993
APPLICATION NUMBER: USN 07/796,066
FILING DATE: 10-ANG-1993
APPLICATION NUMBER: USN 07/796,066
FILING DATE: 20-ANG-1993
APPLICATION NUMBER: USN 07/796,066
FILING DATE: 20-ANG-1994
APPLICATION NUMBER: USN 0
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Best Local Similarity
Matches 302; Conserv
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Patent No. 5882894
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (610)407-0701
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 313 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: n. MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Smith, K. A., & Beadling, C.
TITLE OF INVENTION: Nucleic Acids Encoding CR8 Polypeptide, Vector and
TITLE OF INVENTION: Transformed Cell Thereof, and Expression Thereof
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Valley Forge
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 313 amino a TYPE: peptide STRANDEDNESS: n.a.
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241
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                               PFEHDEEIVKGQVYFRQRVSSECQHLIRWCLSLRPSDRPSFEEIQNHPWMQDVLLPQATA 300
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; STRANDEDNESS: n.a.
; TOPOLOGY: n.a.
; MOLECULE TYPE: peptide
US-08-463-074B-26
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US-08-463-074B-26
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/463,074B
FILING DATE: 5-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/104,736
FILING DATE: 10-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/796,066
FILING DATE: 20-NOV-91
ATTORNEY/AGENT INFORMATION:
NAME: Viviana Amzel, ph. D.
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: 966 38143 (DART-020)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 622-7700
                                                                                                                                                                                                                                                                                                                                                                  Query Match
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
SOFTWARE: Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (213) 622-7700
TELEFAX: (213) 489-4210
INFORMATION FOR SEQ ID NO: 26:
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LENGTH: 313 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Los Angeles
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                               Local Similarity
mes 302; Conserv
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PFEHDEEIVKGQVYFRQRVSSECQHLIRWCLSLRPSDRPSFEEIQNHPWMQDVLLPQATA
                                                                      ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI
                                                                                                                                         ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG
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                                                      ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI
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Pred. No. 6.7e-160;
6; Mismatches 5;
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US-08-465-585C-26
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US-08-465-585C-26
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Matches 302;
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COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PetentIn Release #1.0, Version #1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,585C
FILING DATE: 5-UNUE-1995
PRIOR APPLICATION NUMBER: USSN 08/330,108
APPLICATION NUMBER: USSN 08/330,108
FILING DATE: 27-OCT-1994
APPLICATION NUMBER: USSN 08/104,736
FILING DATE: 10-AUG-1993
APPLICATION NUMBER: USSN 07/796,066
FILING DATE: 20-NOV-1991
ATTORNEY/ACENT INFORMATION:
NUMBER: USSN 07/796,066
FILING DATE: 20-NOV-1991
ATTORNEY/ACENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: Nucleic Acids Encoding CR6 Polypeptide, Vecto TITLE OF INVENTION: Transformed Cell Thereof, and Expression Thereof NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: n. MOLECULE TYPE:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 622-7700
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Viviana Amzel, Ph. REGISTRATION NUMBER: 30,
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Similarity 96.5%;
02; Conservative
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ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI
                   ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI
                                                                     ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180
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Pred. No. 6.7e-160;
6; Mismatches 5;
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US-08-652-446-26
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Patent No.
           NAME: Viviana Amzel, Ph. D.
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: FP66
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 622-7700
TELEFAX: (213) 489-4210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION UNMBER: EP AP
FILING DATE: 5-JAN-1998
APPLICATION NUMBER: ECT/U
FILING DATE: 5-JUN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08
APPLICATION NUMBER: US 08
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                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 08/46
FILING DATE: 5-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/46
FILING DATE: 5-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/46
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APPLICATION NUMBER: 08/
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PRIOR APPLICATION DATA:
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APPLICATION NUMBER: 08/
FILING DATE: 5-JUN-1995
PRIOR APPLICATION DATA:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/46
FILING DATE: 5-JUN-1995
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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TITLE OF INVENTION:
                                                                                                                         FILING DATE: 29-OCT-1996 ATTORNEY/AGENT INFORMATION:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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STATE: California
COUNTRY: USA
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5-JAN-1998
11MBER: PCT/US/96/09194
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Nucleic Acids Encoding CR5
Polypeptide, Vector and Tx
Expression Thereof
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Suite 19

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TYPE: peptide;
STRANDEDNESS: n.a.
TOPOLOGY: n.a.
MOLECULE TYPE: peptide
US-08-652-446-26
                                                                                                                                                                                                                                                                     Sequence 7, Application US/09237543A

Patent No. 6143540
GENERAL INFORMATION:
APPLICANT: KABPALICY, ROSANA
ITITLE OF INVENTION: NOVEL MOLECULES OF THE HK
ITITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: 035800/175631
CURRENT APPLICATION UNMBER: US/09/237,543A
CURRENT FILING DATE: 1999-01-26
NUMBER OF SEQ ID NOS: 11
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 7
LENGTH: 313
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US-09-237-543-7
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Best Local Similarity
Matches 295; Conserv
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Best Local Similarity
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TYPE: P
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                                       ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180
                                                                                         NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL
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ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI
                                                                             NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSDFSGVIRLLDWFERPDSFVLIL
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                        ERPEPVQDLFDFITERGALQEDLARGFFWQVLEAVRHCHNCGVLHRDIKDENILIDLSRG
                                                                                                                               MLLSKINSLAHLRARPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD
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Pred. No. 6.7e-160;
6; Mismatches 5;
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                                                                                                                                                                                Score 1584; DB 2;
Pred. No. 7.5e-156;
8; Mismatches 10;
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                                                                                                                                                                                                         Length 313;
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; LENGTH: 313
; TYPE: PRT
; ORGANISM: Mus r
US-09-644-450-7
                                                                               US-07-857-2248-41
, Sequence 41, Application US/07857224B
, Patent No. 5958784
; GENERAL INFORMATION:
    APPLICANT: Benner, Steven A.
    TITLE OF INVENTION: Predicting Folded Structures
    NUMBER OF SEQUENCES: 114
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US-09-644-450-7
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APPLICANT: Kapeller, Rosana
TITLE OF INVENTION: NOVEL MOLECULES OF THE
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: 035800/175631
CURRENT APPLICATION NUMBER: US/09/644,450
CURRENT FILING DATE: 2000-08-23
NUMBER OF SEQ ID NOS: 11
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SEQ ID NO 7
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Best Local Similarity
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                                                               CORRESPONDENCE ADDRESS:
STREET:
CITY: Z
STATE:
                                 ADDRESSEE: Steven A. Benner Hadlaubstrasse 151
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Pred. No. 7.5e-156;
B; Mismatches 10;
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; Sequence 2, Application US/09237543A
; Batent NO. 6143540
; GENERAL INFORMATION:
APPLICANT: Kappeller, Rosana
: TITLE OF INVENTION: NOVEL MOLECULES OF TH
: TITLE OF INVENTION: AND USES THEREOF
: FILE REFERENCE: 035800/175631
; CURRENT APPLICATION NUMBER: US/09/237,543
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US-09-237-543-2
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Best Local S
Matches 244
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 436
PRIOR APPLICATION DATA: none
TELECOMMUNICATION INFORMATION:
TELEPHONE: (International) 41 1 632 2830
TELEPAX: (International) 41 1 262 2437
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ORIGINAL SOURCE:
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COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette, 1.4 Mb storage
COMPUTER: Apple MacIntosh
OPERATING SYSTEM: MacIntosh 7.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE: Protein kinase; Table 8 Column PUBLICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         JOURNAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AUTHORS: Hanks, S. K.
AUTHORS: Quinn, A. M.
AUTHORS: Hunter, T.
TITLE: The protein kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PAGES: 42-52
DATE: 1988
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/07/857,224B FILING DATE: 03/25/92
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                                                                                                                                                                                                                 PSDRPSFEEIQNHPWMQ 291
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Microsoft Word
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   NUMBER: US/09/237,543A
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94.9%;
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Pred. No. 5.6e-127;
7; Mismatches 3;
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                                                  THE HKID-1-RELATED
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SOFTWARE: PatentIn Ver.
SEQ ID NO 2
LENGTH: 326
TYPE: PRT
ORGANISM: Homo sapiens
US-09-644-450-2
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US-09-644-450-2
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; SOFTWARE: PatentIN Ver. 2.0
; SEQ ID NO 2
; LENGTH: 326
; TYPE: PRT
; ORGANISM: Homo sapiens
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Best Local S
Matches 220
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Patent No. 6383791
GENERAL INFORMATION:
APPLICANT: Kapeller, Rosana
TITLE OF INVENTION: NOVEL MOLECULES OF THE
TITLE OF INVENTION: AND USES THEREOF
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Best Local
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CURRENT APPLICATION NUMBER: US/0:
CURRENT FILING DATE: 2000-08-23
NUMBER OF SEQ ID NOS: 11
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                                                                                                                                                                          Similarity 69.0
20; Conservative
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                                                                                                                                          MLLSKINSLAHLRAAP--CNDLHANKLAPGK-EKEPLESQYQVGPLLGSGGFGSVYSGIR
 FLLVLERPEPAQDLFDFITERGALDEPLARRFFAQVLAAVRHCHSCGVVHRDIKDENLLV
                FVLILERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILI 175
                                                        IADGLPVAVKHVVKERVTEWGSL-GGATVPLEVVLLRKVGAAGGARGVIRLLDWFERPDG
                                                                      VADNLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKV--SSGFSGVIRLLDWFERPDS
                                                                                                                 MLLSKFGSLAHL-CGPGGVDHLPVKILQPAKADKESFEKAYQVGAVLGSGGFGTVYAGSR
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                                                                                                                                                                        68.0%; Score 1135; DB 2; 69.6%; Pred. No. 3.1e-109; 7ative 34; Mismatches 52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          68.0%; Scc
69.6%; Pre
ative 34;
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Pred. No. 3.1e-109;
4; Mismatches 52;
                                                                                                                                                                                                                                                                                                                                                                                                    HKID-1-RELATED PROTEIN FAMILY
                                                                                                                                                                                                    Length 326;
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             Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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length: 2000000000
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1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

3: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*

5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*

6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*
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     US-09-971-791-8
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US-09-971-791-9
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US-10-394-322A-52
US-10-348-081-13
US-10-664-421-15
US-10-664-421-15
US-10-951-406-19
US-10-952A-22
US-09-971-791-7
US-10-348-081-14
US-10-341-635-2
US-10-377-268-10
US-10-664-4221-7
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									ME.	Ĭ.	Simi 3;	Rat	13	rastseQ	SEQ ID NOS:	FILING DATE: 1999-01-26	FILING DATE: 2000-08-23	APPLICATION NUMBER: 09/644,450	FILING DATE:	ENCE	Z		
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	ECOHE	COHL	GTRV	GTRV	ELARS	SLARS	GTRV	GTRV	NKLA	NKLA	Score Pred. Mis			version		1	3	, 450	FILING DATE: 2001-10-04		LES C	Þ	Kosanna Kaperter-Libermann
	PFEHDEEIVKGQVYFRQRVSSECQHLIRWCLSURPSDRPSFEEIQNHPWMQDVLLPQATA	PFEHDEEIVKGQVYFRQRVSSECQHLIRWCLSLRPSDRPSFEEIQNHPWMQDVLLPQATA	ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHGRSAAVWSLGILLYDMVCGDI	ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI	ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG	ERPEPVQDLFDF1TERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG	NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL	NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL	MLLSKINSLAHLRAAPCNDLHANKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD	MLLSKINSLAHLRAAPCNDLHANKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD	core 1668; red. No. 5. Mismatches								16/		OF THE		•
	SLRP	SLRP	SWIRY	WIRY	LEAV	/LEAV	/L'L'K	ווי אל	EPLE	EPLE	1668; DB 3; No. 5.8e-143; matches 0;										E HKI		
	SDRPS	SDRPS	HRYHO	HRYHO	RHCH	RHCH	VSSGI	VSSGI	SQYQV	SQYQ	B 3; -143; 0;										D-1-1		
	SFEET	FEEI	3RSAA	BRSAA	ICGVE	- KG-VL	SGVI	SGVI	/GPLL	GPLL											RELAT		
	QNHPI QHHQ	ONHP	VWSLC	VWSLO	HRDII	HRDI	RLLD	RLLD	GSGGI	GSGGI	Length : Indels										ED P		
	AMQDV	VODV	ATTIE	ATTIE	KDENI	- KOENI	WFERF	WEERE	FGSVY	FGSVY	313;										HKID-1-RELATED PROTEIN FAMILY AND USES		
	LT PQ	TT-PQ1	DMVC	DMVC	TIDI	LIDL	DSEV	DSEV	SGIR	SGIR	Gaps										N FA		
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	300	300	240	240	180	180	120	120	60	60	0,										AND		
																					Sasn		

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APPLICANT: GRUENENTHAL GMBH

TITLE OF INVENTION: SCREENING METHOD USING PIM1-KINASE OR PIM3-KINASE

FILE REFERENCE: 029310.52818US

CURRENT APPLICATION NUMBER: US/10/705,757

CURRENT FILING DATE: 2003-11-12

PRIOR APPLICATION NUMBER: PCT/EP02/05234

PRIOR APPLICATION NUMBER: DE 101 23 055.9

PRIOR APPLICATION NUMBER: DE 101 23 055.9

PRIOR RILING DATE: 2001-05-11

NUMBER OF SEQ ID NOS: 11

SOPTWARE: Patentin Ver. 2.1

SEQ ID NO 4

LENGTH: 313

TYPE: PRT
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US-10-705-757-4
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TYPE: PRT
; ORGANISM: Rattus norvegicus
US-10-348-081-12
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US-10-348-081-12
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APPLICANT: TSCHANK, Georg
TITLE OF INVENTION: PIM-3 KINASE AS A TARGET FOR TYPE 2 DIABETES MELLITUS
FILE REFERENCE: DEAV2302/0004 US NP
CURRENT APPLICATION NUMBER: US/10/348,081
CURRENT FILING DATE: 2003-01-21
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PAtentin version 3.2
SEQ ID NO 12
                                                                                                                                                                                                                                      Sequence 4, Application US/10705757 Publication No. US20040146942A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 12, Application US/10348081 Publication No. US20040038246A1 GENERAL INFORMATION:
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Best Local Similarity
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ORGANISM: Rattus norvegicus
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100.0%; Pred. No. 5.8e-143;
artice n. Mismarches 0;
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; TYPE: PRT
; ORGANISM: Homo s
US-09-971-791-9
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US-09-971-791-9
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Best Local Similarity
Matches 313; Conserv
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Best Local Similarity 97.1%;
Matches 304; Conservative 6
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Sequence 9, Application US/09971791
; Sequence 9, Application US/09971791
; GENERAL INFORMATION:
; APPLICANT: Rosanna Kapeller-Libermann
; APPLICANT: Kyle MacBelher-Dwen
; APPLICANT: Kyle MacBelh
; TITLE OF INVENTION: NOVEL MOLECULES OF THE HKID-1-RELATED PROTEIN FAMILY AND USES THE
; FILE REFERENCE: 35800/23856
; CURRENT APPLICATION NUMBER: US/09/971,791
; CURRENT APPLICATION NUMBER: 09/644,450
; PRIOR APPLICATION NUMBER: 09/644,450
; PRIOR APPLICATION NUMBER: 09/237,543
; PRIOR APPLICATION NUMBER: 09/237,543
; PRIOR FILING DATE: 2000-08-23
; PRIOR FILING DATE: 1999-01-26
; SOFTWARE: FastSEQ for Windows Version 4.0
; SOFTWARE: FastSEQ for Windows Version 4.0
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                           ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI
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100.0%; Score 1668; DB 4; ilarity 100.0%; Pred. No. 5.8e-143; Conservative 0; Mismatches 0;
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Pred. No. 4.7e-140;
6; Mismatches 3;
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RESULT 6
US-10-394-322A-52
Sequence 52, Application US/10394322A
Publication No. US20030232391A1
Publication No. US20030232391A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: SURESIS PHARMACEUTICALS, INC.
APPLICANT: PRESCOLL, John C.
TITLE OF INVENTION: IDENTIFICATION OF KINASE INHIBITORS
FILE REFERENCE: 39750-0006 US
CURRENT APPLICATION NUMBER: US/10/394,322A
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US-10-081-119-18
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Publication No. US20030045491A1
GENERAL INFORMATION:
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SEQ ID NO 18
LENCTH: 313
TYPE: PRT
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Best Local Similarity 97.1%;
Matches 304; Conservative (
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CURRENT APPLICATION NUMBER: US/10/081,119
CURRENT FILING DATE: 2002-02-21
PRIOR APPLICATION NUMBER: 60/289,813
PRIOR FILING DATE: 2001-02-21
NUMBER OF SEQ ID NOS: 38
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APPLICANT: Jefferson, Anne B.
APPLICANT: Chan, Vivien W.
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Pred. No. 4.7e-140;
6; Mismatches 3;
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Best Local S
Matches 304
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APPLICANT: TSCHANK, Georg
TITLE OF INVENTION: PIM-3 KINASE AS A TARGET FOR TYPE 2 DIABETES MELLITUS
FILE REFERENCE: DEAV2002/0004 US NP
CURRENT APPLICATION NUMBER: US/10/348,081
CURRENT FILING DATE: 2003-01-21
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin version 3.2
SEQ ID NO 13
SEC ID NO 13
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PRIOR APPLICATION NUMBER: US 60/366,89
PRIOR FILING DATE: 2002-03-21
NUMBER OF SEQ ID NOS: 70
SOFTWARE: FASTSEQ for Windows Version
SEQ ID NO 52
LENGTH: 313
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Best Local :
                                                                                                                  Matches 304;
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Pred. No. 4.7e-140;
6; Mismatches 3;
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Pred. No. 4.7e-140;
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APPLICANT: IBRAHIM, PRABHA
APPLICANT: IBRAHIM, PRABHA
APPLICANT: KUMAR, ABHINAV
APPLICANT: MANDIYAN, VALSAN
APPLICANT: MANDIYAN, VALSAN
APPLICANT: MILBURN, MICHAEL V.
TITLE OF INVENTION: CRYSTAL STRUCTURE OF PIM-1 KINASE
FILE REFERENCE: 039363/0703
CURRENT APPLICATION NUMBER: US/10/664,421
CURRENT APPLICATION NUMBER: 60/412,341
PRIOR APPLICATION NUMBER: 60/412,341
PRIOR APPLICATION NUMBER: 60/412,341
PRIOR FILING DATE: 2002-09-20
PRIOR APPLICATION NUMBER: 60/411,398
PRIOR FILING DATE: 2002-09-16
NUMBER OF SEQ ID NOS: 169
SOFTWARE: Patentin Ver. 3.2
SEQ ID NO 1
LENGTH: 313
TYPE: PRT
ORGANISM: Homo Bapiens
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Best Local Similarity
Matches 304; Conserv
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EIHLHSLSPGPSK 313
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RESULT

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Sequence 150. Application US/10664421

Publication No. US20040142864A1

GENERAL INFORMATION:
APPLICANT: BREMER, RYAN
APPLICANT: IBRAHIM, PRABHA
APPLICANT: KUMAR, ABHINAV
APPLICANT: MANDIYAN, VALSAN
APPLICANT: MANDIYAN, WALSAN
APPLICANT: MICHAEL V.
APPLICANT: MILBURN, MICHAEL V.
ITILE OF INVENTION: CRYSTAL STRUCTURE OF PIM-1 KINASE
FILE REFERENCE: 039363/0703

CURRENT APPLICATION NUMBER: US/10/664,421

CURRENT APPLICATION NUMBER: 60/412,341

PRIOR APPLICATION NUMBER: 60/412,341

PRIOR APPLICATION NUMBER: 60/412,341

PRIOR APPLICATION NUMBER: 60/411,398

PRIOR PILING DATE: 2002-09-16

PRIOR APPLICATION NUMBER: 60/411,398

PRIOR PILING DATE: 2002-09-16

VUMBER OF SEQ ID NOS: 169

SOFTWARE: Patentin Ver. 3.2

LENGTH: 313

TYPE: PAT

CORGANISM: Homo sapiens
GENERAL INFORMATION:

APPLICANT: GRUERENTHAL GMH

TITLE OF INVENTION: SCREENING METHOD USING PIM1-KINASE OR PIM

FILE REFERENCE: 029310.52818US

CURRENT APPLICATION NUMBER: US/10/705,757

CURRENT FILING DATE: 2003-11-12

PRIOR APPLICATION NUMBER: PCT/EP02/05234

PRIOR FILING DATE: 2002-05-13

PRIOR FILING DATE: 2002-05-13

PRIOR FILING DATE: 2001-05-11

NUMBER OF SEQ ID NOS: 11

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 2

LENGTH: 313
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US-10-705-757-2
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Best Local Similarity 97.1%;
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Pred. No. 4.7e-140;
6; Mismatches 3;
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APPLICANT: HIRTH, KLAUS-PETER
APPLICANT: MILBURN, MICHAEL VANCE
ITITLE OF INVENTION: METHOD FOR THE DESIGN OF MOLECULAR SCAFFOLDS AND LIGANDS
ITILE REFERENCE: 039363/0303
CURRENT APPLICATION NUMBER: US/10/377,268
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: 60/437,929
PRIOR APPLICATION NUMBER: 60/437,929
PRIOR APPLICATION NUMBER: 60/437,929
PRIOR APPLICATION NUMBER: 60/430,651
PRIOR APPLICATION NUMBER: 60/411,398
PRIOR APPLICATION NUMBER: 60/411,398
PRIOR APPLICATION NUMBER: 60/411,398
PRIOR APPLICATION NUMBER: 60/412,341
PRIOR FILING DATE: 2002-09-16
PRIOR FILING DATE: 2002-09-20
NUMBER OF SEQ ID NOS: 38
COPETMANDE DATE: 2002-09-20
                                                                                                                                                                                                           LENGTH: 313
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-377-268-9
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US-10-377-268-9
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Best Local S
Matches 304
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SEQ ID NO 9
LENGTH: 313
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Best Local Similarity
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Pred. No. 4.7e-140;
6; Mismatches 3;
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Pred. No. 4.7e-140;
6; Mismatches 3;
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RESULT 13
US-10-951-406-18
; Sequence 18, Application US/10951406
; Publication No. US20050059630A1
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Sequence 18, Application US/10951389
Publication No. US20050058627A1
GENERAL INFORMATION:
APPLICANT: Reinhard, Christoph
APPLICANT: Chan, Vivien W.
TITLE OF INVENTION: TTK in Diagnosis and as a 7
TITLE OF INVENTION: TTK in Cancer
FILE REFERENCE: 16932.002
CURRENT APPLICATION UNMBER: US/10/951,389
CURRENT FILING DATE: 2004-09-27
PRIOR APPLICATION NUMBER: US/10/081,119
PRIOR FILING DATE: 2002-02-21
PRIOR APPLICATION NUMBER: 60/289,813
PRIOR APPLICATION NUMBER: 60/289,813
PRIOR FILING DATE: 2001-02-21
NUMBER OF SEQ ID NOS: 38
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 18
LENGTH: 313
TYDE: DRT
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EIHLHSLSPSPSK
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Pred. No. 4.7e-140;
6; Mismatches 3;
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APPLICANT: Reinhard, Christoph
APPLICANT: Jefferson, Anne B.
APPLICANT: Jefferson, Anne B.
APPLICANT: Chan, Vivien W.
TITLE OF INVENTION: TTK in Diagnosis and as a Therapeutic TITLE OF INVENTION: Target in Cancer FILE REFERENCE: 16932.002
CURRENT APPLICATION NUMBER: US/10/951,477
CURRENT FILING DATE: 2004-09-27
PRIOR APPLICATION NUMBER: US/10/081,119
PRIOR APPLICATION NUMBER: US/10/081,119
PRIOR APPLICATION NUMBER: 05/289,813
PRIOR APPLICATION NUMBER: 60/289,813
PRIOR APPLICATION NUMBER: 50/289,813
PRIOR FILING DATE: 2001-02-21
NUMBER OF SEQ ID NOS: 38
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 18
LENGTH: 313
TYDE: DET
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APPLICANT: Reinhard, Christoph
APPLICANT: Jefferson, Anne B.
APPLICANT: Chan, Vivien W.
TITLE OF INVENTION: Target in Cancer
FILE REFERENCE: 16932.002
CURRENT APPLICATION NUMBER: US/10/951,406
CURRENT FILING DATE: 2004-09-27
PRIOR APPLICATION NUMBER: US/10/061,119
PRIOR APPLICATION NUMBER: US/10/081,119
PRIOR APPLICATION NUMBER: 00/289,813
PRIOR FILING DATE: 2001-02-21
PRIOR FILING DATE: 2001-02-21
NUMBER OF SEG ID NOS: 38
SOFTWARE: FRASTSEQ for Windows Version 4.0
SEG ID NO 18
LENGTH: 313
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US-10-951-477-18
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                                                                                                                                                                                                                                                                                                                                    Sequence 18, Application US/10951477
Publication No. US20050063974A1
GENERAL INFORMATION:
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Best Local :
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ORGANISM: Homo sapiens
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Pred. No. 4.7e-140;
6; Mismatches 3;
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PRIOR APPLICATION NUMBER: 10/081,119
PRIOR FILING DATE: 2002-02-21
PRIOR FILING DATE: 2001-02-21
PRIOR FILING DATE: 2001-02-21
PRIOR APPLICATION NUMBER: 10/360,848
PRIOR APPLICATION NUMBER: 09/570,593
PRIOR APPLICATION NUMBER: 09/570,593
PRIOR APPLICATION NUMBER: 09/570,593
PRIOR FILING DATE: 2000-05-12
PRIOR APPLICATION NUMBER: 10/763,692
PRIOR PILLING DATE: 1999-05-14
PRIOR PILLING DATE: 2004-01-22
PRIOR APPLICATION NUMBER: 09/626,301
PRIOR PILLING DATE: 2000-07-25
PRIOR APPLICATION NUMBER: 60/148,936
PRIOR APPLICATION NUMBER: 60/148,936
PRIOR APPLICATION NUMBER: 60/145,612
PRIOR APPLICATION NUMBER: 60/145,612
PRIOR FILLING DATE: 1999-08-13
PRIOR FILLING DATE: 1999-08-13
PRIOR PILLING DATE: 1999-08-13
PRIOR PILLING DATE: 1999-07-26
PRIOR PILLING DATE: 2003-10-30
PRIOR FILLING DATE: 2003-10-30

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US-10-977-087-18
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APPLICANT: Reinhard, Christoph
APPLICANT: Jefferson, Anne B.
APPLICANT: Chan, Vivien W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 18, Application US/10977087 Publication No. US20050130926A1
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APPLICANT: Khoja, Hamiduddin
APPLICANT: Shyamala, Venkatakrishna
APPLICANT: Shyamala, Venkatakrishna
TITLE OF INVENTION: GENE PRODUCTS DIFFERENTIALLY EXPRESSED IN CANCEROUS CELLS
TITLE OF INVENTION: AND THEIR METHODS OF USE V
FILE REFERENCE: 2300-21186
CURRENT APPLICATION NUMBER: US/10/977,087
CURRENT FILING DATE: 2004-10-28
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Pred. No. 4.7e-140;
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-977-087-18
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1: /SIDSS/ptodata/2/pubpaa/US06_NEW_PUB.pep1:*

2: /SIDSS/ptodata/2/pubpaa/US06_NEW_PUB.pep:*

3: /SIDSS/ptodata/2/pubpaa/US07_NEW_PUB.pep:*

4: /SIDSS/ptodata/2/pubpaa/US08_NEW_PUB.pep:*

5: /SIDSS/ptodata/2/pubpaa/US08_NEW_PUB.pep:*

6: /SIDSS/ptodata/2/pubpaa/US09_NEW_PUB.pep:*

7: /SIDSS/ptodata/2/pubpaa/US09_NEW_PUB.pep:*

8: /SIDSS/ptodata/2/pubpaa/US10_NEW_PUB.pep:*

9: /SIDSS/ptodata/2/pubpaa/US10_NEW_PUB.pep:*

10: /SIDSS/ptodata/2/pubpaa/US11_NEW_PUB.pep:*

11: /SIDSS/ptodata/2/pubpaa/US11_NEW_PUB.pep:*

12: /SIDSS/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
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Copyright (c) 1993 - 2006 Biocceleration Ltd
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944.812 Million cell updates/sec
                Sequence 373, App
Sequence 2982, Ap
Sequence 32, Appl
Sequence 40, Appl
Sequence 690, Appl
Sequence 74, Appl
Sequence 74, Appl
Sequence 115, Appl
Sequence 11, Appl
Sequence 1231, Appl
Sequence 1231, Appl
Sequence 1231, Appl
Sequence 3611, Appl
Sequence 3997, Appl
Sequence 37, Appl
Sequence 37, Appl
Sequence 22124, A
Sequence 22124, A
Sequence 22124, A
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Publication No. US20060084066A1

GENERAL INFORMATION:

APPLICANT: Biogen Idec

TITLE OF INVENTION: Surrogate Markers of Pain
FILE REFERENCE: 08201.6029-00000

CURRENT APPLICATION NUMBER: US/10/784,004

CURRENT FILING DATE: 2004-02-20

NUMBER OF SEQ ID NOS: 1251

SOFTWARE: PatentIn version 3.2

SEQ ID NO 373

LENGTH: 455

TYPE: PRT

ORGANISM: rat
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US-10-370-959-31	US-10-370-959-17 .	35	US-11-087-099-7631	US-11-151-601-4	US-11-096-568A-20430	US-11-096-568A-20431	US-11-087-099-1845	US-11-096-568A-18364	US-10-979-095-6	US-11-087-099-3898	US-10-204-639-65	US-11-087-099-1886	US-10-204-639-17	US-11-096-568A-32575	US-10-995-561-877	US-10-995-561-876	US-10-995-561-880	US-10-995-561-878	US-10-995-561-881	US-11-087-099-12402	US-11-177-138-10	US-10-770-726-67	US-10-784-004-951
31,	17, App	83	7631		2043	æ	1845,	e 18	6, App	e 38	Sequence 65, Appl	e 18	17,	e 3257	877,	876,		878,	881,	124	Sequence 10, Appl	Sequence 67, Appl	Sequence 951, App

## ALIGNMENTS

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Query Match 67.8%; Score 1131.5; D
Best Local Similarity 72.5%; Pred. No. 3e-89;
Matches 214; Conservative 30; Mismatches
                                                                                       176
 368
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FVLILERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILI
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APPLICANT: MORTIS, MACDONALD
APPLICANT: ROSENDERG, Steven
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
TITLE OF INVENTION: METHODS AND COMPOSITION FOR DIAGNOSING
TITLE OF INVENTION: METHODS AND COMPOSITION FOR DIAGNOSING
TITLE OF INVENTION: METHODS AND COMPOSITION TRANSPLANT REJECTION
FILE REPERENCE: 506612000104
CURRENT APPLICATION NUMBER: US/10/511,937
CURRENT FILING DATE: 2004-10-19
PRIOR APPLICATION NUMBER: US/10/131,831
PRIOR FILING DATE: 2003-04-24
PRIOR APPLICATION NUMBER: US/10/131,831
PRIOR APPLICATION NUMBER: US/10/131,831
PRIOR APPLICATION NUMBER: US/10/131,831
PRIOR APPLICATION NUMBER: US/10/131,831
PRIOR FILING DATE: 2002-04-24
PRIOR APPLICATION NUMBER: US/10/1325,899
PRIOR FILING DATE: 2002-04-24
PRIOR APPLICATION NUMBER: US/10/1325,899
PRIOR FILING DATE: 2002-12-20
NUMBER OF SEQ ID NOS: 3117
SOFTWARE: PATENTIN Version 3.2
SEQ ID NO 2982
US-10-511-937-2982
                                                                            Sequence 32, Application US/10501841
Publication No. US20060084055A1
GENERAL INFORMATION:
APPLICANT: Gaiger, Alexander
APPLICANT: Algate, Paul A.
APPLICANT: Mannion, Jane
APPLICANT: Clapper, Jonathan David
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US-10-501-841-32
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 55.9
Matches 170; Conservative
                                                          APPLICANT:
APPLICANT:
APPLICANT:
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                      APPLICANT:
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Woodward, Robert
Ly, Ngoc
Prentice, James
MacDonald
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Ordonez, Nadia
Carter, Lauren
McNeill, Patricia Dianne
                                                          Clapper, Jor
Wang, Aijun
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APPLICANT: Carper, Conscious David
APPLICANT: Wang, Aljun
APPLICANT: Carter, Lauren
APPLICANT: McNeill, Patricia Dianne
APPLICANT: McNeill, Patricia Dianne
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Compositions and Methods for the Detection, Dia-
TITLE OF INVENTION: and Therapy of Hematological Malignancies
FILE REFERENCE: 014058-014402PC
CURRENT APPLICATION NUMBER: US/10/501,841
CURRENT APPLICATION NUMBER: US/10/501,841
CURRENT FILING DATE: 2003-01-22
PRIOR APPLICATION NUMBER: WO PCT/US03/02353
PRIOR APPLICATION NUMBER: WO PCT/US03/02353
PRIOR APPLICATION NUMBER: WO PCT/US03/02353
PRIOR FILING DATE: 2003-01-22
NUMBER OF SEQ ID NOS: 124
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 4
US-10-501-841-40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 52.1%; Score 869; DB 9; Best Local Similarity 55.9%; Pred. No. 6.5e-67;
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TITLE OF INVENTION: Compositions and Methods for the Detection,
TITLE OF INVENTION: and Therapy of Hematological Malignancies
FILE REFERENCE: 014058-014402PC
CURRENT APPLICATION NUMBER: US/10/501,841
CURRENT FILING DATE: 2004-07-14
PRIOR APPLICATION NUMBER: US 10/057,475
PRIOR FILING DATE: 2002-01-22
PRIOR FILING DATE: 2003-01-22
NUMBER OF SEQ ID NUMBER: WO PCT/US03/02353
PRIOR FILING DATE: 2003-01-22
NUMBER OF SEQ ID NOS: 124
NUMBER OF SEQ ID NOS: 124
NUMBER OF SEQ ID NOS: 124
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                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Gaiger, Alexander APPLICANT: Algate, Paul A.
                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Mannion, Jane
APPLICANT: Clapper, Jonathan David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               202
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    262 LIRRCLAPKPSSRPSLEEILLDPWMQTPAEDVTPQPLQRRPCPFGLVLATLSLAWPGLAP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                82 LEVALLWKVGAGGGHPGVIRLLDWFETQEGFMLVLERPLPAQDLFDYITEKGPLGEGPSR
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TITLE OF INVENTION: 2150, Human Protein Kinase Fan
TITLE OF INVENTION: Member and Uses Therefor
FILE REFERENCE: MPI2001-137P1RNM
CURRENT APPLICATION NUMBER: US/11/103,065
CURRENT FILING DATE: 2005-04-11
PRIOR APPLICATION NUMBER: US/10/184,563
PRIOR APPLICATION NUMBER: US/10/184,563
PRIOR APPLICATION NUMBER: 00/301,702
PRIOR FILING DATE: 2001-06-28
PRIOR FILING DATE: 2001-06-28
NUMBER OF SEQ ID NOS: 7
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; ORGANISM: Homo sapiens
US-10-501-841-40
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US-11-103-065-2
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Best Local Simi
Matches 166;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: FastSEQ
SEQ ID NO 2
LENGTH: 311
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                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Homo sapiens
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Local Similarity 58.0%;
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                                                                             SFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRGELKLIDFGSGALLKDTVYTDFDCTR
                                                                                                                                                                                        GKEKEPLESQYQVGPLLGSGGFGSVYSGIRVADNLPVAIKHVEKDRISDWGELPNGTRVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDIPFEHDEEIVKGQVYFRQRVSSECQH 265
                                                                                                                           LEVALLWKVGAGGGHPGVIRLLDWFETQEGFMLVLERPLPAQDLFDYITEKGPLGEGPSR
                                                                                                                                                         MEVVLLKKVSS--GFSGVIRLLDWFERPDSFVLILERPEPVQDLFDFITERGALQEELAR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LIRRCLAPKPSSRPSLEEILLDPWMQ---TPAEDVPLNPSKGGPAP 304
VYSPPEWISRHQYHALPATVWSLGILLYDMVCGDIPFERDQEILEAELHFPAHVSPDCCA
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                                                                                                                                                                                                                                                                                                                                                                                                           for Windows Version
                                                                                                                                                                                                                                                         51.9%; Score 866.5; DB 11; 58.0%; Pred. No. 9.7e-67; tive 41; Mismatches 74;
                                                                                                                                                                                                                                                        41;
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Sequence 690, Application US/10505928

Sequence 690, Application US/10505928

Publication No. US20060088532A1

GENERAL INFORMATION:
APPLICANT: Ludwig Institute for Cancer Research et TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES FILE REFERENCE: 28967/39178

CURRENT APPLICATION NUMBER: US/10/505,928

CURRENT FILING DATE: 2004-08-27

PRIOR APPLICATION NUMBER: US 60/363,019

PRIOR FILING DATE: 2002-03-07

NUMBER OF SEQ ID NOS: 866

SOFTWARE: PATENT APPLICATION SEG ID NOS: 866

SOFTWARE: PATENT APPLICATION SEG ID NOS: 866

SEQ ID NO 690

LENGTH: 661

TYPE: PRT

ORGANIAN: Homo sapiens

US-10-505-928-690
                                                                                                                                                                                                                                                            Sequence 74, Application US/10877346
Publication No. US20060014153A1
GENERAL INFORMATION:
APPLICANT: Gerlach, Valerie L
APPLICANT: MacDougall, John R
APPLICANT: Smithson, Glennda
APPLICANT: Millet, Isabelle
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US-10-877-346-74
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APPLICANT:
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Best Local Similarity
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APPLICANT:
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APPLICANT:
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                                     APPLICANT:
CANT: Shimkets, Richard A OF INVENTION: Novel Proteins REFERENCE: 21402-124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  266 LIRWCLSLRPSDRPSFEEIQNHPWMQDVLLPQATAEIHLHSLSPSP 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          262 LIRRCLAPKPSSRPSLEEILLDPWMQ---TPAEDVPLNPSKGGPAP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KEPLESQYQVGPLLGSGGFGSVYSGIRVADNLPVAIKHVEKDRISDWGELPNGTRVPMEV
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                                                       Kekuda, Ramesh
Spytek, Kimberly A
Leach, Martin D
                                                                                                                                                                 Ellerman, Karen
Grosse, William M
Alsobrook II, John P
                                                                                                                                                                                                                                            Millet, Isabe
Stone, David
                                                                                                                                Lepley, Denise M
Burgess, Catherine
                                                                                                                                                                                                                            Gunther, Erik
                                                                                                              Padigaru, Muralidhara
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                     and Nucleic
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                     Acids
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RESULT 8
US-11-087-099-9816
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CURRENT FILING DATE: 2004-06-25
PRIOR APPLICATION NUMBER: US/09/964,956
PRIOR FILING DATE: 2001-09-26
PRIOR FILING DATE: 2000-09-27
PRIOR PELLING DATE: 2000-09-27
PRIOR FILING DATE: 2000-09-27
PRIOR FILING DATE: 2000-09-27
PRIOR PELLING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: 60/235,633
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: 60/236,064
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: 60/236,065
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: 60/236,066
PRIOR PILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: 60/236,066
PRIOR PILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: 60/236,135
PRIOR FILING DATE: 2000-09-28
PRIOR FILING DATE: 2000-09-28
PRIOR FILING DATE: 2000-09-29
PRIOR APPLICATION NUMBER: 60/236,331
PRIOR PILING DATE: 2000-10-05
PRIOR FILING DATE: 2000-10-05
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               APPLICANT: Abad, Mark S. et al.
TITLE OF INVENTION: Genes and Uses for Plant Improvement
FILE REFERENCE: 38-21 (53450)B EP
CURRENT APPLICATION NUMBER: US/11/087,099
CURRENT FILING DATE: 2005-03-22
NUMBER OF SEQ ID NOS: 12464
SEQ ID NO 9816
LENGTH: 504
                                                                                                                                                                                    Sequence 9816, Application US/11087099 Publication No. US20060041961A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 96; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Ver. SEQ ID NO 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: Description of Artificial Sequence: OTHER INFORMATION: domain Consensus Sequence:-10-877-346-74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Remaining Prior Application data removed - NUMBER OF SEQ ID NOS: 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 256
                                                                                                                                                                                                                                                                                                                                                                                     265
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 157 HCHNCGVLHRDIKDENILIDLNRGELKLIDFGSGALLKDTVY---TDFDGTRVYSPPEWI 213
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       38 YQVGPLLGSGGFGSYYSGIRVADNLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 YELGEKLGSGAFGKVYKGKHKDTGEIVÄIKILKKRSLSE-----KKKRFLREIQILRRLS
                                                                                                                                                                                                                                                                                                                                         HLIRWCLSLRPSDRPSFEEIQNHPW 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RYHRYHGRSAAVWSLGILLYDMVCGDIPF---EHDEEIVKGQVYFRQRV-----SSECQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YLHSRGIVHRDLKPENILLDEN-GTVKIADFGLARKLESSSYEKLTTFVGTPEYMAPEVL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    --HPNIVRLLGVFEEDDHLYLVMEYMEG-GDLFDYLRRNGLLLSEKEAKKIALQILRGLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22.7%; Score 378.5; DB 36.2%; Pred. No. 5e-25; tive 49; Mismatches 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         See
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; ORGANISM: Homo
US-10-501-035-357
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276
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GENERAL INFORMATION:

APPLICANT: Bristol-Myers Squibb Company

ITILE OF INVENTION: IDENTIFICATION OF POLYNUCLEOTIDES AND POLYPEPTIDE FOR

ITILE OF INVENTION: ACTIVITY OF COMPOUNDS THAT INTERACT WITH PROTEIN TYRO

ITILE OF INVENTION: ACTIVITY OF COMPOUNDS THAT INTERACT WITH PROTEIN TYRO

ITILE OF INVENTION: AND/OR PROTEIN TYROSINE KINASE PATHWAYS

FILE REFERENCE: D0185 PCT

CURRENT APPLICATION NUMBER: US/10/501,035

CURRENT FILING DATE: 2004-07-09

PRIOR APPLICATION NUMBER: US 60/350,061

PRIOR APPLICATION NUMBER: US 60/350,061

PRIOR FILING DATE: 2002-01-18

NUMBER OF SEQ ID NOS: 795

SOFTWARE: PATENTIN VERSION 3.2

SEQ ID NO 357

LENGTH: 950
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 90; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 87; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          38 YQVGPLLGSGGFGSYYSGIRVADNLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MLVVDPMKRITIPEIRQHPWFQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLSLRPSDRPSFEEIQNHPWMQ 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LYAGPEVDVWSCGVILYALLCGTLPFD-DENIPNLFKKIKGGIYTLPSHLSSGARELIPS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              --HPHIRTYEVIETPSDIYVVMEYVKS-GELFDYIVEKGRLQEDEARNFFQQIISGVEY
                                                                                                                                                                                                                                         CHNCGVLHRDIKDENILIDLNRGELKLIDFGSGALLKD-TVYTDFDGTRVYSPPEWIRYH
                                                                                                                                                                                                                                                                                                                   --HPHIIKLYQVMETKSMLYLVTEYAKN-GEIFDYLANHGRLNESEARRKFWQILSAVDY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RYHGRSAAVWSLGILLYDMVCGDIPFEHDEEI-----VKGQVY-FRQRVSSECQHLIRW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YOVGPLLGSGGFGSVYSGIRVADNLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVS
LVLDPSKRLTIAQIKEHKWMLIEVPVQRPVLYPQ
                                                 LSLRPSDRPSFEEIQNHPWM-----QDVLLPQ
                                                                                                     QYEGPQLDIWSMGVVLYVLVCGALPFDGPTLPILRQRVLEGRFRIPYFMSEDCEHLIRRM
                                                                                                                                                         RYHGRSAAVWSLGILLYDMVCGDIPFEHD-----EEIVKGQVYFRQRVSSECQHLIRWC
                                                                                                                                                                                                             CHGRKIVHRDLKAENLLLD-NNMNIKIADFGFGNFFKSGELLATWCGSPPYAAPEVFEGQ
                                                                                                                                                                                                                                                                                                                                                                    SGFSGVIRLLDWFERPDSFVLILERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRH 157
                                                                                                                                                                                                                                                                                                                                                                                                                        YDIEGTLGKGNFAVVKLGRHRITKTEVAIKIIDKSQL----DAVNLEKIYREVQIMKMLD
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31.8%; Pred. No. 2.5e-23;
ative 52; Mismatches 113
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Pred. No. 1.1e-23;
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RESULT 10 US-11-241-056-11

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                                                                                                                           ; TYPE: PRT ; ORGANISM: Lycopersicon esculentum US-11-087-099-11500
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US-11-087-099-11500
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                                                                                                                                                                                     APPLICANT: Abad, Mark S. et al.
TITLE OF INVENTION: Genes and Uses for Plant Improvement
FILE REFERENCE: 38-21(53450)B EP
CURRENT APPLICATION NUMBER: US/11/087,099
CURRENT FILING DATE: 2005-03-22
NUMBER OF SEQ ID NOS: 12464
SEQ ID NO 11500
LENGTH: 514
                                                                                                                                                                                                                                                                                                                                                                              Sequence 11500, Application US/11087099
Publication No. US20060041961A1
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SOFTWARE: Patentin version 3.1
SEQ ID NO 11
LENGTH: 631
                                         Matches
                                                                                 Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Anderson, Dirk M.
TITLE OF INVENTION: NOVEL MURINE AND HUMAN KINASES
FILE REFERENCE: 2933-US
CURRENT APPLICATION NUMBER: US/11/241,056
CURRENT FILING DATE: 2005-09-30
PRIOR APPLICATION NUMBER: US/09/980,464
PRIOR PILIAGION NUMBER: US/09/980,464
PRIOR FILING DATE: 2001-11-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Immunex Corporation APPLICANT: Bird, Timothy A. APPLICANT: Virca, G. Duke APPLICANT: Martin, Unja
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Mus musculus
                                       Local Similarity
tes 87; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  244 -HDEEIVKGQV----YFRQRVSSECQHLIRWCLSLRPSDRPSFEEIQNHPWM 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        83
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38 YQVGPLLGSGGFGSVYSGIRVADNLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVS 97
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R-GDLYDYISERPRLSERDARHFFROIVSALHYCHQNGIVHRDLKLENILLDAN-GNIKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRGELKL 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IDFG-SGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDIPFE 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLILERPE 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ANKLAPGKEKEP--------LESQYQVGPLLGSGGFGSVYSGIRVADNLPV 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADFGLSNLYHKGKFLQTFCGSPLYASPEIVNGKPYVGPEVDSWSLGVLLYILVHGTMPFD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AIKSIRKDKIKDEQDL---LHIRREIEIMS--SLNHPHIIAIHEVFENSSKIVIVMEYAS 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ARPLADGLIKSPKPLMKKQAVKRHHHKHNLRHRYEFLETLGKGTYGKVKKA-RESSGRLV
                                         Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21.9%; Score 364.5; DB 11; 32.9%; Pred. No. 2.4e-23;
                                     21.5%; Score 358; DB 11; 33.2%; Pred. No. 6.8e-23; tive 54; Mismatches 105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       49;
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                                       105;
                                                                             Length 514;
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                                   Gaps
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PRIOR APPLICATION NUMBER: 60/235,631
PRIOR FILING DATE: 2000-09-27
PRIOR PPLICATION NUMBER: 60/235,633
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: 60/235,808
PRIOR APPLICATION NUMBER: 60/235,808
PRIOR FILING DATE: 2000-09-27
PRIOR FILING DATE: 2000-09-27
              SOFTWARE: PatentIn Ver.
SEQ ID NO 72
LENGTH: 256
TYPE: PRT
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                                                                                    Remaining Prior Application data removed NUMBER OF SEQ ID NOS: 127
                                                                                                                       PRIOR APPLICATION NUMBER: 60/
PRIOR FILING DATE: 2000-10-05
                                                                                                                                                                                                  PRIOR
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PRIOR APPLICATION NUMBER: US/09/964,956
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/10/877,346
CURRENT FILING DATE: 2004-06-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Shimkets, Richard A
TITLE OF INVENTION: Novel Proteins and Nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILE REFERENCE: 21402-124
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ORGANISM: Artificial Sequence
                                                                                                                                                           APPLICATION NUMBER: 60/237,434 FILING DATE: 2000-10-03
                                                                                                                                                                                                                 APPLICATION NUMBER: 60/236,135
                                                                                                                                                                                                                                  APPLICATION NUMBER: 60/236,066 FILING DATE: 2000-09-27
                                                                                                                                                                                                 FILING DATE: 2000-09-28
                                                                                                                                                                                                                                                                      FILING DATE: 2000-09-
                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 60/236,064
                                                                                                                                                                                                                                                                                     APPLICATION NUMBER:
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Smithson, Glennda
Millet, Isabelle
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ellerman, Karen
Grosse, William M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gunther, Erik
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lepley, Denise M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Martin D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              David
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Kimberly A
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                                                                                                                                        60/238,321
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OTHER INFORMATION:
OTHER INFORMATION:
US-11-113-424-183
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US-11-113-424-183
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PRIOR FILING DATE: 2000-12-19
PRIOR PELICATION NUMBER: 60/311,590
PRIOR FILING DATE: 2001-08-10
PRIOR FILING DATE: 2000-12-20
PRIOR PELICATION NUMBER: 60/257,314
PRIOR PELICATION NUMBER: 60/311,613
PRIOR PELICATION NUMBER: 60/311,613
PRIOR FILING DATE: 2001-08-10
PRIOR PELICATION NUMBER: 60/315,617
PRIOR PELICATION NUMBER: 60/307,506
PRIOR FILING DATE: 2001-07-24
PRIOR FILING DATE: 2001-07-24
PRIOR FILING DATE: 2001-07-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 183, Application US/11113424
Publication No. US20050260713A1
GENERAL INFORMATION:
APPLICANT: Gangolli et al.
TITLE OF INVENTION: Polypeptides and Nucleic Acids
FILE REFERENCE: 21402-225
CURRENT APPLICATION NUMBER: US/11/113,424
CURRENT FILING DATE: 2005-04-21
                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 190
SOFTWARE: PatentIn Ver. 2
SEQ ID NO 183
LENGTH: 256
               Query Match
Best Local Similarity
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                                                                                                                                   ORGANISM: Artificial Sequence FEATURE:
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                                                                                                                                                                                                                                                       FILING DATE: 2001-05-29
APPLICATION NUMBER: 60/288,153
FILING DATE: 2001-05-02
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   Conservative
                                                                                         Description of Artificial Sequence: consensus sequence
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21.3%; Score 355.5; DB
33.0%; Pred. No. 4.7e-23
cive 56; Mismatches 9
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Pred. No. 4.7e-23;
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                                   DB 11;
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Sequence 12331, Application US/11087099

Publication No. US20060041961A1

GENERAL INFORMATION:
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TITLE OF INVENTION: Genes and Uses for Plant
FILE REFERENCE: 38-21(53450) B EP
CURRENT APPLICATION NUMBER: US/11/087,099
CURRENT FILING DATE: 2005-03-22
NUMBER OF SEQ ID NOS: 12464
SEQ ID NO 12331
LENGTH: 504
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Pred. No. 2.9e-22;
3; Mismatches 112;
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RESULT 15
US-11-087-099-3997
; Sequence 3997, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:

APPLICANT: Abad, Mark S.

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Search completed: May 4, Job time: 16.3333 secs
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                                                                                                                                                                                                                                                                                                                         Query Match 21.0%; Score 350; DB 11; Length 512; Best Local Similarity 31.7%; Pred. No. 3.3e-22; Matches 84; Conservative 60; Mismatches 99; Indels 22;
                                                                               267
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## ALIGNMENTS

HKID-1; serine/threonine kinase; cellular proliferative disorder; differentiative disorder; cancer; haematopoietic neoplastic disorder; Acute promyeloid leukaemia; APML; Chronic myelogenous leukaemia; CML; ABG33016 standard; protein; 313 Rattus norvegicus. Waldenstrom's macroglobulinaemia; Rat protein kinase phosphorylation site ABG33016; 22-AUG-2002. US2002115120-A1. 20-DEC-2002 (first entry) ₿ WΜ. #2

04-OCT-2001; 2001US-00971791.

26-JAN-1999; 99US-00237543 23-AUG-2000; 2000US-00644450 99US-00237543.

(MILL-) MILLENNIUM PHARM INC.

Kapeller-Libermann R, Rudolph-Owen LA, Macbeth

WPI; 2002-712471/77.

Modulating levels or activity of HKID-1 polypeptides, a member of serine/threonine kinase superfamily, for treating cancer, by contacell expressing the polypeptide with a modulator of the polypeptid r, by contacting polypeptide.

Example 3; Page 39-40; 48pp; English.

The invention describes a method of modulating the level or activity of human HKID-1 polypeptide, a member of serine/threonine kinase superfamily. The method involves contacting a cell expressing the polypeptide or nucleic acid with an agent to modulate the level or activity of polypeptide, or level of nucleic acid molecule. The method is useful for modulating the level or activity of HKID-1 polypeptide or polypucleotide in a subject having or predisposed to having a disorder involving cancer. Modulating HKID-1 expression or activity is useful for therapeutic purposes, for treating cellular proliferative and/or

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The present invention relates to a method of identifying pain-regulating compounds, involving screening candidate compounds for interaction with
                                                                         Claim 1;
                                                                                                                     Method for identifying analgesics, useful particularly for treating chronic pain, by screening compounds for interaction with PIM-1 or kinase, or related compounds.
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Pred. No. 9.6e-159;
Mismatches 0;
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Best Local S
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                                                                                                                                                                                                                                                                                                                                 04-DEC-2003
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Pred. No. 9.6e-159;
Mismatches 0;
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The present sequence is the protein sequence of protein kinase and proto-oncogene, PIM-1. PIM-1 paralogues of novel human and murine PIM-3 prote
                                                                                                              New human or murine PIM-3 DNAs or po
agent for identifying anti-type 2 di
treating insulin resistance or type
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                                                                                                                                                                                                                                  Mueller
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Best Local Similarity
Matches 313; Conserv
WPI; 2005-556609/57.
N-PSDB; AEB96038.
REFSEQ; NP_058730.
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                                                                                                                                                                                                              30-JAN-2004; 2004DE-10004894
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Pred. No. 9.6e-159;
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Identifying substances that regulate PIM kinases, useful for treatment and diagnosis of urinary incontinence and the urge to urinate, and similar use of PIM proteins or nucleic acids.
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The invention relates to a novel method for identifying substances that regulate urinary incontinence and the urge to urinate. The method comprises incubating a test compound with a cell and/or cell preparation that has synthesized a specific protein of the PIM (proviral integration site) kinase family and measuring either binding of the test compound to the PIM kinase, or a functional parameter that is altered by the binding. The method of the invention demonstrates uropathic and gene therapy applications and may be useful for treatment and diagnosis of urinary incontinence and the urge to urinate. The method is based upon regulating the activity or expression of PIM kinases that are involved in bladder control. The current sequence is that of the Norway rat PIM-1 serine-threenine kinase protein of the invention.

Sequence 313 A A

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9.6e-159;
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ABP54943 standard; protein; 313

ABP54943;

13-JAN-2003 (first entry

Human Pim1.

RESULT 5
ABB549X
XX ABB95
XX ABB95
XX ABB95
XX ABB95
XX ABB96
XX Huma
XX Pinl
KW Pinl
KW Mitc
KW huma
XX Huma
XX Huma
XX W Homc
XX W Homc
XX W Homc
XX W WO20
XX WO20
XX Y Z1-FF Piml; tyrosine threonine kinase; mitotic checkpoint; colon cancer human; gene therapy. TTK; pro protein cancer; tumo enzyme;

Homo sapiens.

WO200268444-A1

06-SEP-2002.

21-FEB-2002; 2002WO-US005278

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RESULT 6
ABG33017
ID ABG3
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AC ABG3
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AC ABG3
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AC HUma
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DT 20-E
XX
DE Huma
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Best Local Simi
Matches 304;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             abnormal expression levels a prostate and ovarian cancer.
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 HKID-1; serine/threonine kinase; cellular proliferative disorder;
                               Human protein kinase phosphorylation site
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(TTK) activity, useful in diagnosing and treating disorders with
all expression levels and activity of TTK, such as lung, colon,
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Pred. No. 1.6e-155;
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Matches 304;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention describes a method of modulating the level or activity of human HKID-1 polypeptide, a member of serine/threonine kinase superfamily. The method involves contacting a cell expressing the polypeptide or nucleic acid with an agent to modulate the level or activity of polypeptide, or level of nucleic acid molecule. The method is useful for modulating the level or activity of HKID-1 polypeptide or polynucleotide in a subject having or predisposed to having a disorder involving cancer. Modulating HKID-1 expression or activity is useful for therapeutic purposes, for treating cellular proliferative and/or differentiative disorders including cancer or haematopoietic neoplastic disorders e.g. Acute promyloid leukaemia (APML), Chronic myelogenous leukaemia (CML) and Waldenstrom's macroglobulinaemia (WM). This is the amino acid sequence of a human protein kinase phosphorylation site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Modulating levels or activity of HKID-1 polypeptides, a member of serine/threonine kinase superfamily, for treating cancer, by contacting cell expressing the polypeptide with a modulator of the polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 differentiative disorder; cancer; Acute promyeloid leukaemia; APML; Waldenstrom's macroglobulinaemia;
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23-AUG-2000; 2000US-00644450
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97.1%;
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Pred. No. 1.6e-155;
6; Mismatches 3;
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RESULT

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Matches 304; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention relates to a method of identifying pain-regulating compounds, involving screening candidate compounds for interaction with PIM1 or PIM3 kinase. PIM1 and PIM3 proteins and coding sequences are useful for treating chronic pain, particularly of neuropathic or inflammatory origin (e.g. where associated with diabetes, cancer, AIDS or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Method for identifying analgesics, useful particularly for treating chronic pain, by screening compounds for interaction with PIM-1 or kinase, or related compounds.
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)B; ABZ69186.
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                                       EIHLHSLSPSPSK 313
                                                                                                                                          PFEHDEEIVKGQVYFRQRVSSECQHLIRWCLSLRPSDRPSFEEIQNHPWMQDVLLPQATA
EIHLHSLSPGPSK 313
                                                                                               PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA
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                                             with an amount of an agent effective to reduce TTK polypeptide activity of a cancerous cell (comprising: (i) detecting the activity of a CTTK polypeptide in the presence of a candidate agent (c) the activity of TTK polypeptide in the presence of a candidate agent (c) capent), identifying an agent that reduces TTK activity of TTK polypeptide activity in the absence of the candidate agent (c) contacting a cancerous cell displaying elevated expression of a TTK contacting a cancerous cell displaying elevated expression of a TTK contacting polymucleotide with a candidate agent; and (ii) comparing the prognosis of a cancerous disease other than ovarian cancer in a control more control comprising: (i) detecting expression of TTK encoding polymucleotide in a test cancer cell of a subject; and (ii) comparing a converse of expression of the polymucleotide in a test cancer cell of a subject; and (ii) comparing a concer cell with a level of expression of the polymucleotide in the test cancer cell with a level of expression of the polymucleotide in a control non-cancer cell is condicative to the level of expression in the control non-cancer cell is condicative of the prognosis of the cancerous disease). The methods are useful for detecting cancer (other than ovarian cancer cell is controling synchrhof cancerous cells, identifying an agent that reduces TTK covarian cancer. The methods are also useful for determining the ability of a subject to respond to a particular therapy e.g. as a basis of correcting the bursey. The present sequence represents a closely related correction to human TTK. in this case human TMM (not defined)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            non-cancer cell, where an increase in the expression level of TTK protein or nucleic acid in the test cell compared to that in the normal cell, indicates the presence of cancer other than ovarian cancer. Also included are reducing growth of a cancerous cell (by contacting a cancerous cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        a subject, comprising comparing the expression levels of tyrosine threonine kinase (TTK, a mitotic checkpoint gene) polypeptide or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Detecting cancer in a subject, by comparing expression levels of tyrosine threonine kinase polypeptide or polynuclectide in a subject cell and a normal cell, where an increase in the expression level in the test cell is indicative of cancer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  threonine kinase (TTK, a mitotic checkpoint gene) polypeptide polynucleotide in a test cell obtained from the subject and in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to detecting cancer (other than ovarian cancer)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 34-35; 79pp; English
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The present sequence is the protein sequence of the human serine/threonine protein kinase and proto-oncogene, PIM-1. PIM-1 protein are the paralogues of novel human and murine PIM-3 proteins (see ABR6293 and ABR6293) of the invention, which are therefore expected to be and ABR62933) of the invention, which are therefore expected to be a livolved in cancer and cell growth regulation. PIM-3 is also involved in the development of insulin resistance and type 2 diabetes mellitus. The invention relates to the use of PIM-3 nucleic acids and proteins in: screening assays for compounds that modulate insulin resistance or type
                                                                                                                                                                                                                                                                               New human or murine PIM-3 DNAs or polypeptides, useful for agent for identifying anti-type 2 diabetes mellitus drugs, treating insulin resistance or type 2 diabetes mellitus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABR62939 standard; protein; 313
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                                                                                                                                                                                                                                 Example 2; Page 40; 40pp; English.
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                                                                                                                                                                                                                                                  Human; pain; neuronal tissue; gene therapy; spinal segmental nerve injury; chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
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01-NOV-2001; 2001US-0346382P
26-NOV-2001; 2001US-0333347P
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                                                                                                                                                                                                                                                                                                                                            PFEHDEEIVKGQVYFRQRVSSECQHLIRWCLSLRPSDRPSFEEIQNHPWMQDVLLPQATA
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Pred. No. 1.6e-155;
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention relates to a method for identifying a ligand (I), which binds to an inactive conformation of target protein kinase (T). The method involves contacting inactive conformation of (T), which contains or is modified to contain a reactive group at or near a binding site of interest, with one or more ligand candidates capable of covalently bonding to the reactive group thus forming a kinase-(L) conjugate (C). The method is useful for identifying protein kinase inhibitors that preferentially bind to inactive conformation of a target protein kinase. The present sequence is a protein kinase which may be modified via an amino acid substitution, for use in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 313 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Identifying ligand binding to inactive conformation of target protein kinase (T) comprises contacting the conformation modified (T) which contains reactive group at binding site, with ligands and detecting kinase-ligand conjugate formation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; protein kinase; enzyme; inhibitor; PIM1.
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                                                                                           PFEHDEEIVKGQVYFRQRVSSECQHLIRWCLSLRPSDRPSFEEIQNHPWMQDVLLPQATA
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   EIHLHSLSPGPSK
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                                                                     PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA
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97.1%;
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Pred. No. 1.6e-155;
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Best Local S
Matches 304
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; PRO; immune related disorder; systemic lupus erythematosus; rheumatoid arthritis; osteoarthritis; juvenile chronic arthritis; systemic sclerosis; Sjogren's syndrome; vasculitis; sarcoidosis; autoimmune haemolytic anaemia; autoimmune thrombocytopenia; thyroiditis; autoimmune haemolytic anaemia; autoimmune thrombocytopenia; thyroiditis; diabetes mellitus; renal disease; demyelinating disease; central nervous system; peripheral nervous system; central nervous system; peripheral nervous system;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel PRO polypeptide e.g., PRO69614, PRO71106, or PRO86388 useful for treating an immune related disorder such as systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             06-NOV-2003; 2003WO-US035268
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                                                                                                                                                                                                                                                                                                                                   Sequence 313
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Wu TD;
                                                                                  ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG
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Pred. No. 1.6e-155;
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Best Local S
Matches 304
                                                                                                                                                                                                                                                                                                                                                                                          The present invention relates to a method of designing a ligand binding to a target molecule. The method involves identifying as molecular scaffolds compounds binding to members of a molecular family, detecting orientation of scaffolds at a binding site of target, and synthesising ligand. The invention is useful for designing drug products and for designing ligand binding to target molecules such as nuclear hormone receptors, TNP receptors, G-protein coupled receptors, methyl transferases, ligases, etc. The present sequence is the human PIM 1 protein. This sequence is used to illustrate the method of invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Designing a ligand binding to a target molecule, comprises identifying molecular scaffolds compounds binding to members of a molecular family, detecting orientation of scaffolds at a binding site of target, and synthesizing ligand.
                                                                                                                                                                                                                                                                                                                                           Sequence
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16-SEP-2002; 2002US-04113981P.

20-SEP-2002; 2002US-0412341P.

02-JAN-2003; 2003US-0437929P.
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97.1%;
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Pred. No. 1.6e
6; Mismatches
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            antiinflammatory, antiarthritic, antirheumatic, immunosuppressive, costeopathic, antialabetic, dermatological, antippressive, antialabetic, dermatological, antippressive, antialabetic, antialabetic, antippressive, antialabetic, antialabetic, antippressive, and respiratory activity. A polynucleotide of the invention may have a use in gene therapy. The PRO polypeptide, its agonist, antagonist, or antibody that specifically binds to the polyneptide is useful for treating an immune related disorder such as systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, osteoarthritis, or idiopathic chronic arthritis, a spondyloarthropathy, systemic sclerosis, and idiopathic inflammatory myopathy. Sjogren's syndrome, systemic conditis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes mellitus, immune-mediated renal disease, a demyelinating disease of the central or peripheral nervous system, diopathic demyelinating polyneuropathy, a hepatobiliary disease, infectious or autoimmune chronic active hepatitis, primary confidence in the contral or cholescope in t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New PRO polypeptides and polynucleotides, useful for treating e.g. erythematosus, rheumatoid arthritis, diabetes mellitus, immune-mediated renal disease, or demyelinating diseases of the central or peripheral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRO; antiinflammatory; antiarthritic; antirheumatic; immunosuppressive; osteopathic; antidiabetic; dermatological; antipsoriatic; antiallergic; antiasthmatic; hepatotropic; respiratory; gene therapy; immune system.
                                                                                                                                                                                                                                                                                                                                                antiinflammatory,
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 7;
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                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to
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DB; ADP24226.
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                                                                                                                                                                                                                                                                                                                                              ed by it. A protein of the invention has antiarthritic, antirheumatic, immunosupp
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Best Local
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                      WPI; 2004-748778/73.
N-PSDB; ADT07366.
                                                                                                            03-APR-2003;
                                                                                                                                                             21-OCT-2004
                                                                                                                                                                                                                                                                                                                                            ADT07365
                                                           Kobayashi M,
                                                                                                                                     05-APR-2004; 2004WO-JP004917
                                                                                                                                                                                      WO2004090158-A1
                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                     anticancer
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                                                                                                                                                                                                                                                                                          Human protein
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                                                                                                                                                                                                                                                                                                                                                                   ADT07365 standard; protein;
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                                                                                   (ONCO-) ONCOREX INC.
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Pred. No. 1.6e-155;
6; Mismatches 3;
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Pim-1; cancer;
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Screening

for a prophylactic-therapeutic apoptosis inducing agent

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Search completed: May 4, 2006, 05:24:47 Job time : 114.667 secs
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Best Local Similarity
Matches 304; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to a method of screening a prophylactic-therapeutic agent for an apoptosis inducing agent or an enhancer of an anticancer agent. The method involves the use of a serine/threonine kinase Pim-1, its partial peptide or its salt. Also disclosed is a kit for carrying out the method of the invention. The method is a wesful for screening a prophylactic-therapeutic agent for cancer. The method is also useful for prophylactis and/or treatment of cancer, inducing apoptosis, treating a patient having a solid tumour that is resistant to an anticancer agent (induced by hypoxia), and for screening a substance that promotes or inhibits the activity of serine/threonine kinase Pim-1. The present sequence represents a human polypeptide relating to the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 313 AA;
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al Similarity 97.1%;
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Pred. No. 1.6e-155;
6; Mismatches 3;
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serine/threonine p
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probable serine/th
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p69E33 protein - A
serine/threonine-s
hypothetical prote
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probable protein k
probable serine/th
probable serine/th
Ca2+/calmodulin-de
SNF-related kinase
serine/threonine-s
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321.5	323.5	324.5	325	325	325.5	326	328	328	330	331.5	333	333	333.5	333.5
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480	713	423	1246	513	774	591	745	442	461	520	502	435	746	339
ν.	٥ -	2	N	-	N	N	N	N	N	N	N	N	N	N
A86427	T37886	T40224	G89287	860303	I48609	S54788	G01025	T48203	T14822	G86414	T02306	E84707	S62365	S56719
probable serine/th	probable serine/th	protein kinase – f	protein H39E23.1 (	serine/threonine-s	probable serine/th	calcium-stimulated	serine/threonine p	hypothetical prote	probable serine/th	probable protein k	probable protein k	probable protein k	SNF1-related prote	serine/threonine-s

## ALIGNMENTS

RESULT 1 S26298 S76298 Protein kin N/Alternate C/Species: C/Date: 25- C/Accession R/Wingett Nucleic Aci A/Title: Ch A/Reference A/Accession A/Molecule A/Molecule A/Molecule A/Molecule A/Molecule A/Molecule A/Molecule A/Coss-ref A/Cross-ref A/Cros	RESULT 1  S26298  protein kinase (EC 2.7.1.37) pim-1 - rat  protein pim-1 pim-1 proto-oncogene proi  protein pim-1; pim-1 pim-1 pim-1; pim-
R; Wingett Nucleic A A; Title: A; Referen A; Accessi A: Molecul	in
A;Molecul A;Residue A;Cross-r	26794; UNIPARC:UPI0000131AD6;
A; Experim A; Note: t C; Comment	tal source: testis tis-specific transcript is shorter and more stal Pim-1 autophosphorylates at unknown sites.
C; Function A; Descrip	n: .ion: catalyzes the formation of peptidyl-serine-phosphate or
A; Note: i	testis may be involved in signal transduction events of norm
C; Keyword	C;Reywords: ATP; autophosphorylation; phosphoprotein; phosphotransferase; proto-oncogen
F;36-290/ F;44-52/R F;67/Acti	F;36-290/Domain: protein kinase homology <kin> F;44-52/Region: protein kinase ATP-binding motif F;67/Active site: Lys #status predicted</kin>
Query Match Best Local Matches 31	Query Match 100.0%; Score 1668; DB 1; Length 313; Best Local Similarity 100.0%; Pred. No. 2.6e-74; Matches 313; Conservative 0; Mismatches 0; Indels 0; Gaps
Q	MLLSKINSLAHLRAAPCNDLHANKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD
מם	1 MLLSKINSLAHLRAAPCNDLHANKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD
γ	61 NLPVAIKHVEKDRISDWGELFNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL
מם	61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL
8	121 ERPEPVODLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG
DЬ	
Ş	181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI
מם	181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPBWIRYHRYHGRSAAVWSLGILLYDMVCGDI
φ	241 PFEHDEEIVKGQVYFRQRVSSECQHLIRWCLSLRPSDRPSFEEIQNHPWMQDVLLPQATA
дb	241 PFEHDEEIVKGQVYFRQRVSSECQHLIRWCLSLRPSDRPSFEEIQNHPWMQDVLLPQATA
δ	301 EIHLHSLSPSPSK 313

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C;Species: Homo sapiens (man)
C;Abte: 31-Mar-1989 #sequence_revision 07-Oct-1994 #text_change
C;Abte: 31-Mar-1989 #sequence_revision 07-Oct-1994 #text_change
C;Abte: 31-Mar-1989 #sequence_revision 07-Oct-1994
R;Reeves, R.; Spies, G.A.; Kiefer, M.; Barr, P.J.; Power, M.
Gene 90, 303-307, 1990
A;Title: Primary structure of the putative human oncogene, pim-1
A;Reference number: JU0327; MUID:90382681; PMID:2205533
A;Accession: JU0327
                                                                                                                                                                                                                                                                                                                                                                                                            A;Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threoning;Superfamily: kinase-related transforming protein; protein kinase homology C;Keywords: ATP; autophosphorylation; phosphoprotein; phosphotransferase; proto-oncogene F;36-290/Domain: protein kinase homology <KIN> P;44-52/Region: protein kinase ATP-binding motif F;67/Active site: Lys #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Molecule type: mRNA
A;Residues: 1-14, 'RA-',17-313 <ZAK>
A;Residues: 1-14, 'RA-',17-313 <ZAK>
A;Residues: 1-14, 'RA-',17-313 <ZAK>
A;Residues: 1-14, 'RA-',17-313 <ZAK>
A;Residues: 1-14, 'RA-',17-313 <ZAK-', 'GB:M16750; NID:g189956; PIDN:AAA60089.1;
A;Domen, J.; Von Lindern, M.; Hermans, A.; Breuer, M.; Grosveld, G.; Berns, A.A.
Oncogene Res. 1, 103-112, 1987
A;Title: Comparison of the human and mouse PIM-1 cDNAs: Nucleotide sequence and immu A;Reference number: 158412; MUID:88217305; PMID:3329709
A;Accession: 158412
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A;Title: The cDNA sequence and gene analysis A;Reference number: A27476; MUID:87277423; PN A;Accession: A27476
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A;Residues: 1-313 <MEE>
A;Cross-references: UNIPARC:UPI0000001060; GB:M24779;
A;Cross-references: UNIPARC:UPI0000001060; GB:M24779;
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A;Residues: 1-313 <REE>
A;Residues: 1-313 <REE>
A;Cross-references: UNIPROT:P11309; UNIPARC:UPI0000001060;
A;Cross-references: UNIPROT:P11309; UNIPARC:UPI0000001060;
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A;Cross-references: GDB:119495; OMIM:164960

A;Map position: 6p21.2-6p21.2

A;Introns: 28/2; 63/3; 80/3; 203/1; 262/1
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J. Cell. Biochem. 35, 105-112, 1987
A;Title: Cloning and characterization of the human PIM-1 gene: a putative oncogene relat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein kinase
N;Alternate nam
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: UNIPARC:UPI000001060; GB:M54915; C;Comment: Pim-1 autophosphorylates at unknown sites.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: mRNA
A; Residues: 1-313 < DOM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Reference number: A46554; MUID:88115604; PMID:3429489 A;Accession: A46554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: mRNA
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Best Local S
Matches 304
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  ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG
                                                                                                                                                                                                             (EC 2.7.1.37) pim-1 - human
nes: kinase-related transforming protein pim-1; pim-1 proto-oncogene
                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                        98.1%;
97.1%;
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                                                                                                                                                                                                                                                                                                               Score 1636; D
Pred. No. 9.2e
6; Mismatches
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RESULT S55333

4

protein kinase

pim-2

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2.7.1.-) -

mouse

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Cell 46, 603-611, 1986
A;Title: The primary structure of the putative oncogene pim-1 shows extensive homology w A;Reference number: A24169; MUID:86272109; PMID:3015420
A;Reference number: A24169; MUID:86272109; PMID:3015420
A;Reference number: A24169
A;Accession: A24169
A;Accession: A24169
A;Accession: A24169
A;Accession: A24169
A;Accession: I-313 <SEL-
A;Cross references: UNIPROT:P06803; UNIPARC:UPI00000294AF; GB:M13945; GB:M13946; NID:920
C;Comment: Pim-1 autophosphorylates at unknown sites.
C;Comment: Pim-1 autophosphorylates at unknown sites.
C;Gene: pim-1
A;Introns: 28/1; 63/3; 80/3; 203/1; 262/1
C;Function:
A;Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonin C;Superfamily: kinase-related transforming protein; protein kinase homology
C;Reywords: ATP; autophosphorylation; phosphotransferase; proto-oncogene; serine/threonif; 67/Active site: Lys #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein kinase (EC 2.7.1.37) pim-1 - mouse
N;Alternate names: kinase-related transforming protein pim-1; pim-1 proto-oncogene
C;Species: Mus musculus (house mouse)
C;Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 09-Jul-2004
C;Accession: A24169
C;Accession: A24169
C;Species, G; Cuypers, H.T.; Boelens, W.; Robanus-Maandag, E.; Verbeek, J.; Domen,
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Local Similarity 94.2%;
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EIHLHSLSPGSSK
                                      EIHLHSLSPSPSK 313
                                                                            PFEHDEEIIKGQVFFRQTVSSECQHLIKWCLSLRPSDRPSFEEIRNHPWMQGDLLPQAAS
                                                                                                 PFEHDEEIVKGQVYFRQRVSSECQHLIRWCLSLRPSDRPSFEEIQNHPWMQDVLLPQATA
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A;Gene: Pim-2
A;Map position: X
A;Start codon: CTG
A;Note: locus between A-raf and Act-7, near Kv4.1
C;Function:
A;Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threoning;Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threoning;Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threoning;Description: protein kinase forming protein; protein kinase homology
C;Keywords: alternative initiators; ATP; autophosphorylation; phosphoprotein; phosphotraf;89-345/Domain: protein kinase homology <KIN>
F;89-345/Domain: protein kinase ATP-binding motif
F;97-105/Region: protein kinase ATP-binding motif
F;120/Active site: Lys #status predicted
                                                                                       hypothetical protein F45H7.4 - Caenorhabditis C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-C;Accession: T22255 # R;Percy, C.
submitted to the EMBL Data A; Reference number: Z19538 A; Accession: T2255 A; Status: preliminary; tran A; Molecule type: DNA
                                                                                                                                                                                        RESULT
T22255
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EMBO J. 14, 2536-2544, 1995
A;Title: Proviral tagging in E-mu-myc transgenic mice lacking
A;Reference number: S55333; MUID:95300786; PMID:7781606
A;Accession: S55333
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C;Comment: Pim-2 autophosphorylates
C;Genetics:
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A;Molecule type: mRNA
A;Residues: 'M',61-370 <VA3>
A;Cross-references: UNIPARC:UPI00000278BF;
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A;Molecule type: mRNA
A;Residues: 'M',27-370 <VA2>
A;Cross-references: UNIPARC:UPI00000278BE;
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A; Residues: 1-370 < VAN>
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Pred. No. 5.4e.
40; Mismatches
                   from
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                   GB/EMBL/DDBJ
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RESULT 6
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A; Introns: 72/3; 160/3;
C; Superfamily: nroth:
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                                                                                                                                                                                                                                                        C;Genetics:
A;Gene: CESP:C06E8.3
A:Gene: CESP:C06E8.3
A:Thtrons: 24/1; 76/3; 107/2; 145/3; 199/1; 307/1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Residues: 1-363 <WIL>
A;Cross-references: UNIPROT:Q20443; UNIPARC:UPI00001755A4; EMBL:Z34800; A;Experimental source: clone F45H7 C;Genetics: A;Gene: CESP:F45H7.4
                                                                                                                                                                                Ş
                                                                                                                                                                                                                                                                                                                                           A; Residues: 1-409 < FAV > A; Cross-references: UNI
                                                                                                                                                                                                                                                                                                                                                                                                         A; Reference number: A; Accession: T15435
                                                                                                                                                                                                                                                                                                                                                                                                                                  submitted to the EMBL Data Library, Februa A:Description: The sequence of C. elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypothetical protein C06E8.3 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 20-Sep-199 #sequence_revision 20-Sep-1999 #text_change C;Accession: T15435
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Matches 121
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mes 110; Conserv
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                                                                                                                                                                                                                                                                                                                                                                        type: DNA
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                                                     MLLSKINSLAHLRAAPCNDLHANKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RGELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCG
                                    MERPANCMDLFDMVSVHGPLNEDMGKFIFKQVITTVFNMYSKHGLLHRDIKDENLIVNMN
                                                                                                GQQPVAVKFVQHKHVRSW-TMTCRQLIPSEVCHL-ETCEDIPGVIKILDWFANSKGFLIV
                                                                                                                         -NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLI
                                                                                                                                                          MIKRKLQDLAVCCSYQVDFLHEKK----HSVKEFKRKYEVLDEIGRGGFGIVYEATTRQD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LSLRPSDRPSFEEIQNHPWMQDVLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HSLYLGREAAVWSLGVLLYNSLNGRLPFRNEKDICTAHLLGPLPFFVPVSAEVKDLISKC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VHECVQNRVLHRDLKDENIVIDLVTGSTKLIDFGAATVLRRSQYSDFQGTRLYCPPEWFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VRHCHNCGVLHRDIKDENILIDLNRGELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KVSSGFSGVIRLLDWFERPDSFVLILERPEPVQDLFDFITERGALQEELARSFFWQVLEA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LTFDPFQRCSLEAILNHPWVKQQTL
                                                                                                                                                                                                                   29.7%; Score 495; DB 2; llarity 35.3%; Pred. No. 1.6e-17; Conservative 57; Mismatches 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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ce: strain Bristol N2
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9; Mismatches
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175

TGEVKLVDFGATAYAEKATKKEFQGTRSYCPPEWFRDQLYLPLEATSWSLGVLLFILLTG

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R;Ruiz, J.C.; Conlon, F.L.; Robertson, E.J.
Mech. Dev. 48, 153-164, 1994
A;Title: Identification of novel protein kinases expressed
A;Reference number: 149071; MUID:95200798; PMID:7893599
A;Accession: 149072
                                                                                                                                                                                                                                                                                                           RESULT 8
S66730
A;Cross-references:
A;Map position: 15L
C;Keywords: ATP
                                                  A; Molecule type: DNA
A; Residues: 1-1101 <ANS>
A; Cross-references: UNIPROT: Q08217;
A; Experimental source: strain $288C
C; Genetics:
                                                                                                                                                                             C;Accession: S66730 R;Ansorge, W.; Benes, V.; submitted to the Protein
                                                                                                                                                                                                                                hypothetical protein YOL045w - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein O2034
C;Species: Saccharomyces cerevisiae
C;Date: 12-Uul-1996 #sequence_revision 12-Uul-1996 #text_change 05-Oct-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein kinase - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence revision
C;Accession: 149072
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A; Residues: 1-481 < RES >
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                                                                                                                                                            A; Reference number: S66723
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FGSGALLK-DTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDIPFEHD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | SEMFDYLTSNGHLSENEARQKFWQILSAVEYCHNHHIVHRDLKTENLLLDSNM-DIKLAD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      FGFGNFYKPGEPLSTCVGSPPYAAPEVFEGKEYEGPQLDVWSLGVVLYVLVCGSLPFDGP
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                                     SGD: S0005405
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; Pred. No. 8.4e-12;
53; Mismatches 116;
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                                                                                          UNIPARC: UPI000012DF35;
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                                                                                                                                                                                                Schwager,
                                                                                                                                                                               wager, C.;
July 1996
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A;Introns: 205/3; 227/1; 322/3; 688/3; A;Note: EG:22E5.8
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A; Residues: 1-1398 < MUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Description: Sequencing the distal X chromosome o A;Reference number: 217668 A;Accession: T11741 A;Status: preliminary; translated from GB/EMBL/DDBJA;Status: preliminary;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;Murphy, L.; Harris, D.; Barrell, B. submitted to the EMBL Data Library, April 1999 A;Description: Sequencing the distal X chromosome
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                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
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                                         362
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                                                                                                                                                                                                                                                                                                                                                                    29
                                                                                                                                                                                                                                                                                                                                                                                                      91;
                                                                                                                                             VYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDIPFEHD-----EEIVKGQVYFRQRV
                                                                                                                                                                                  KFWQIISAVEYCHKKGIVHRDLKAENLLLDLNM-NIKIADFGFSNHFKPGELLATWCGSP
                                                                                                                                                                                                                                                        YREVEIMKRLK--HPHIIKLYQVMETKNMIYIVSEYASQ-GEIFDYIAKYGRMSESAARF
                                                                                                                                                                                                                                                                                            PMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLILERPEPVQDLFDFITERGALQEELARS 146
                                                                                                                                                                                                                                                                                                                                  KLKEPMRVGFYDIERTIGKGNFAVVKLARHRITKN-EVAIKIIDKSQL-----DQTNLQKV
                                                                                                                                                                                                                                                                                                                                                                KEKEPLE-SQYQVGPLLGSGGFGSV-YSGIRVADNLPVAIKHVEKDRISDWGELPNGTRV
                                         SSECEHLIRRMLVLEPTRRYTIDQIKRHRWMCPELL
                                                                     SSECOHLIRWCLSLRPSDRPSFEEIQNHPWMQDVLL
                                                                                                           PYAAPEVFEGKQYTGPEIDIWSLGVVLYVLVCGALPFDGSTLQSLRDRVLSGRFRIPFFM
                                                                                                                                                                                                                    FFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRGELKLIDFG-SGALLKDTVYTDFDGTR 205
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                                                                                                                                                                                                                                                                                                                                                                                                      57;
                                                                                                                                                                                                                                                                                                                                                                                                      Score 374; DB 2;
Pred. No. 3.2e-11;
57; Mismatches 110
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782/3; 814/2; 1363/3

ę,

Drosophila

melanogaster

#text\_change 09-Jul-2004

110;

18;

Gaps

185

242

Length 1398; Indels

295

259

301

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F;839-1099/Domain: protein kinase homology <KIN>F;847-855/Region: protein kinase ATP-binding motif
                                                                                                                                                         SLIKRILTREVDKRPTIDEIYEDKWLK 1100
                                        HLIRWCLSLRPSDRPSFEEIQNHPWMQ 291
                                                                           YSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDIPFEHDEEIVKGQVYF--RQRVSSECQ 264
                                                                                                                                                                                                                                            ATLNKNSQENILKLLDFFEDDDYYYI----ETPVHGETGSIDLFDVIEFKKDMVEHEAKL
                                                                                                                                                                                                                                                                                  KKVS-SGFSGVIRLLDWFERPDSFVLILERPEPVQ-----DLFDFITERGALQEELARS
                                                                                                                                                                                                                                                                                                                          SDFTILOVMGEGAYGKVNLCIHNREHYIVVIKMIFKERILVDTWVRDRKLGTIPSEIQIM
                                                                                                                                                                                                                                                                                                                                                                SQYQVGPLLGSGGFGSVYSGIRVADNLPVAIKHVEKDRI--SDWGELPNGTRVPMEVVLL
                                                                                                                                                                                                                                                                                                                                                                                                          62;
                                                                                                                                                                                                                                                                                                                                                                                                                           Score 374; DB 2;
Pred. No. 2.6e-11;
                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches 103;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 1101;
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                                                                                                                                                                                                                                                                                        146
                                                                                                                                                                                                                                                                                                                                                                    93
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10

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probable serine/threonine protein kinase (EC 2.7.1.-) - yeast (Saccharomyces cerevisiae)
N.Alternate names: protein YAL002; protein YAL017w; secretory protein SSP138
C;Species: Saccharomyces cerevisiae
C;Date: 30-Sep-1993 #sequence revision 02-Aug-1994 #text_change 05-Oct-2004
C;Accession: S33653; S36717; S36732; JH0486
R;Clark, M.W.; Zhong, W.W.; Keng, T.; Storms, R.K.; Ouellette, B.F.F.; Barton, A.; Kabac
Yeast 9, 543-549, 1993
A;Title: The YAL017 gene on the left arm of chromosome I of Saccharomyces cerevisiae end
A;Reference number: S33653; MUID:93311122; PMID:8322517
A;Accession: S33653; MUID:93311122; PMID:8322517
A;Accession: S3653; MUID:93311122; PMID:8322517
A;Accession: S3653; MUID:93311122; PMID:8322517
A;Cross-references: UNIPROT:P31374; UNIPARC:UPI000017A449; EMBL:L05146
A;Cross-references: UNIPROT:P31374; UNIPARC:UPI000017A449; EMBL:L05146
R;Colerte, F.; Clark, M.W.; Keng, T.; Storms, R.K.; Zhong, W.; Zeng, B.; Fortin, N.; E
Submitted to the EMBL Date Library, January 1993
A;Reference number: S36711
A;Accession: S36711
A;Accession: S36717
A;Molecule type: DNA
A;Residues: 1-664,867-1358 <OUE>
A;Clark, M.W.; Zhong, W.W.; Keng, T.; Storms, R.K.; Barton, A.; Kaback, D.B.; Bussey, H.
Yeast 8, 133-145, 1992
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S33653
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C;Accessi
R;Gumpel,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Residues: 1-504 GUM>
A;Cross references: UNIPROT:P93113;
A;Experimental source: cv. Masterpie C;Function:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       probable serine/threonine-specific protein kinase N;Alternate names: SNF1-related protein kinase C;Species: Cucumis sativus (cucumber) C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: mRNA
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34.4%;
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Pred. No. 3e-11;
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A;Molecule type: DNA
A;Residues: 1-72,'E',74-154 <SID>
A;Cross-references: UNIPARC:UPI000017A44B
C;Genetics:
A;Gene: SGD:FUN31; SSP138
A;Cross-references: SGD:S0000015; MIPS:YALO:
A;Kap position: 1L
C;Keywords: ATP; glycoprotein; phosphotrans:F;1096-1356/Domain: protein kinase homology
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R;Sidhu, R.S.; Mathewes, S.; Bollon, A.P.
Gene 107, 111-118, 1991
A;Title: Selection of secretory protein-encoding genes l
A;Reference number: JH0483; MUID:92077420; PMID:1743509
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Best Local S
Matches 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;Reywords: ATP, glycoprotein; phosphotransferase; serine/threonine-specific;11096-1315/Domain: protein kinase homology <KIN>
;11094-1112/Region: protein kinase ATP-binding motif
;8,128/Binding site: carbohydrate (Asn) (covalent) #status predicted
;1232/Active site: Asp #status predicted
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                                                                          1279
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                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                          GNPYEGQPQDIWAIGILLYTVVFKENPFYNIDEILEGDLKFNNAEEVSEDCIELIKSILN
                                                                                                    YHRYHGRSAAVWSLGILLYDMVCGDIPFEHDEEIVKGQVYFR--QRVSSECQHLIRWCLS
                                                                                                                                                     VRHCHNCGVLHRDIKDENILIDLNRGELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIR
                                                                                                                                                                                                                                 ENILRLLDFFEDDDYYYI----ETPVHGETGCIDLFDLIEFKTNMTEFEAKLIFKQVVAG
                                                                                                                                                                                                                                                                                                            MGEGAYGKVNLCIHKKNRYIVVIKMIFKERILVDTWVRDRKLGTIPSEIQIMATLNKKPH
  RCVPKRPTIDDINNDKWL
                                    LRPSDRPSFEEIQNHPWM
                                                                                                                                                                                                                                                                    SGVIRLLDWFERPDSFVLILERPEPVQ-----DLFDFITERGALQEELARSFFWQVLEA
                                                                                                                                                                                                                                                                                                                                                  LGSGGFGSVYSGIRVADNLPVAIKHVEKDRI--SDWGELPNGTRVPMEVVLLKKVS-SGF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            not shown
                                                                                                                                                                                                                                                                                                                                                                                                           21.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               a Saccharomyces cerevisiae homolog of the SNF2 transcription MUID:92221690; PMID:1561836
                                                                                                                                                                                                                                                                                                                                                                                           56
•
                                      290
                                                                                                                                                                                                                                                                                                                                                                                       Score 366; DB 2;
Pred. No. 7.7e-11;
6; Mismatches 100
                                                                                                                                                                                                                                                                                                                                                                                         100;
                                                                                                                                                                                                                                                                                                                                                                                                                           Length 1358;
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A;Reference number: JC1446; MUID:93013041; F A;Accession: JC1446 serine/threonine-specific protein kinase (EC 2.7.1.-)
N;Alternate names: protein kinase NRI homology
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #tc
C;Accession: JC1446; S58266; S66334
B:LCTOP A; Molecule 1 A; Residues: A; Reference number: S58256 A; Accession: S58266 A;Cross-references: UNIPROT:Q38997; UNIPARC:UPI000012DE43; R;Thuemmler, F.; Kirchner, M.; Teuber, R.; Dittrich, P. submitted to the EMBL Data Library, May 1995 A; Molecule type: DNA A; Residues: 1-512 < LEG> R;LeGuen, L.; Thomas, M.; Bianchi, Gene 120, 249-254, 1992 A; Status: preliminary A; Description: Differential 12 accumulation M.; Halford, of the e from Arabidopsis PMID:1339373 N.G.; Kreis, transcripts #text\_change AK21 -GB:M93023; õ thaliana Arabidopsis 22 novel NID:g166599; encoding protein thaliana

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PIDN

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C;Function:
A,Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonin, A,Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonin C;Superfamily: SNF1-related protein kinase; protein kinase homology
C;Keywords: ATP; magnesium; phosphotransferase; serine/threonine-specific protein kinase F;17-271/Domain: protein kinase homology <KIN>
F;25-33/Region: protein kinase ATP-binding motif
F;48,67,142,144/Active site: Lys, Glu, Asp, Lys #status predicted
F;147,151/Binding site: magnesium (Asn, Asp) #status predicted
                                                                                                                                                                                                              A; Accession type: mRNA
A; Molecule type: mRNA
A; Residues: 1-798 < XIA>
A; Cross-references: UNIPROT: 09IA88; UNIPARC: UPI0000044792; GB: AF219232
A; Cross-references: UNIPROT of the AMPK/SNF1 family of serine/th:
                                                                                                                                                                                                                                                                                                                                                     R;Xia, Y.; Zhang, Z.; Kruse, U.; Vogt, P.K.; Li, J. Biochem. Biophys. Res. Commun. 276, 564-570, 2000 A;Title: The new serine-threonine kinase, Qik, is a target A;Reference number: JC7500 A;Contents: Embryo fibroblasts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 qik protein - chicken
,Alternate names: Qin-induced kinase
C;Species: Gallus gallus (chicken)
C;Date: 17-Nov-2000 #sequence_revision 17-Nov-2000 #text_change 09-Jul-2004
C;Accession: JC7500
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A;Title: Differential accumulation of the transcripts of 22 novel protein kinase genes A;Reference number: S66314; MUID:96123233; PMID:8534852
A;Accession: S66334
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A;Residues: 144-198 <TH2>
A;Cross-references: UNIPARC:UPI000009DEE0; EMBL:X86966; NID:g928909; PIDN:CAA60529.1;
C;Comment: This enzyme plays an important role in a signal transduction cascade regula
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A;Introns: 64/1; 125/3; 186/3; 230/3; 292/3; 322/3;
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Best Local Similarity
Matches 90; Conserv
                                               Matches
                                                                                                                                                      Keywords: protein kinase
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                                                                            Query Match
Best Local (
                                                                            Local Similarity
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                                                    84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LEAVRHCHNCGVLHRDIKDENILIDLNRGELKLIDFGSGALLKDTVYTDFD-GTRVYSPF : | : | : | : | : | : | : | : | : |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LLKKVSSGFSGVIRLLDWFERPDSFVLILERPEPVQDLFDFITERGALQEELARSFFWQV 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ESILPNYKLGRTLGIGSFGRVKIAEHALTGHKVAIKILNRRKIKN---MEMEEKVRREIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EPLESQYQVGPLLGSGGFGSVYSGIRVADNLPVAIKHVEKDRISDWGELPNGTRVPMEVV
  YQVGPLLGSGGFGSVYSGIRVADNLFVAIKHVEKDRISDWGELFNGTRVFMEVVLLKKVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RDLÍ PRMĽVVDPMKŘVTI PE I RQHPWFQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QHLIRWCLSLRPSDRPSFEEIQNHPWMQ 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EVISGKLYAGPEVDVWSCGVILYALLCGTLPFD-DENIPNLFKKIKGGIYTLPSHLSPGA 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EWIRYHRYHGRSAAVWSLGILLYDMVCGDIPFEHDEEI-----VKGQVY-FRQRVSSEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ILRLFM--HPHIIRLYEVIÉTPTDIYLVMEYVNS-GELFDYIVEKGRLQEDEARNFFQQI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ISGVEYCHRNMVVHRDLKPENLLLD-SKCNVKIADFGLSNIMRDGHFLKTSCGSPNYAAP
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                                                    Conservative
                                                                          21.4%;
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33.6%; Pred. No. 5.9e-11;
tive 51; Mismatches 111;
                                                  51;
                                                                            Score 357.5; DB 2;
Pred. No. 1.3e-10;
                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        272
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                                                    Indels
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RESULT S52244

15

p69Eg3 protein

African clawed

frog

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R;Bhalerao, R.P.; Salchert, K.; Bako, L.; Okresz, L.; Szabados, L.; Muranaka, Proc. Natl. Acad. Sci. U.S.A. 96, 5322-7, 1999
A,Title: Regulatory interaction of PRL1 WD protein with Arabidopsis SNP1-like A;Reference number: Z25116; MUID:99238528; PMID:10220464
A;Accession: T52633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       serine/threonine-specific protein kinase (EC 2.7.1.-) AKIN11 [validated] - N.Alternate names: SNF1 protein kinase omolog AKIN11 C.Species: Arabidopsis thaliana (mouse-ear cress) C.Date: 24-Oct-2000 #sequence_revision 24-Oct-2000 #text_change 05-Oct-2004 C.Accession: T52633
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: UNIPROT:P92958; UNIPARC:UPI00000AC16D; A;Experimental source: cultivar Columbia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Gene: AKIN11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Residues: 1-512 <BHA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 90; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;Genetics:
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246
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                                                                                                                                                                                                 LEAVRHCHNCGVLHRDIKDENILIDLNRGELKLIDFGSGALLKDTVYTDFD-GTRVYSPP
                                                                                                                                                                                                                                                                              LIKKVSSGFSGVIRLLDWFERPDSFVLILERPEPVQDLFDFITERGALQEELARSFFWQV 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LVVDPTKRITISQIKQHKWMQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EYEGPHLDIWSLGVVLYVLVCGSLPFDGPNLPTLRQRVLEGRFRIPYFMSEDCETLIRRM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YDIERTLGKGNFAVVKLARHRVTKTQVAIKIIDKTRL---DPSNLEKIYREVQIMKLLN
RDLIPRMLIVDPVKRITIPEIRQHRWFQ
                                     QHLIRWCLSLRPSDRPSFEEIQNHPWMQ 291
                                                                             EVISGKLYAGPEVDVWSCGVILYALLCGTLPFD-DENIPNLFKKIKGGIYTLPSHLSSEA
                                                                                                                   EWIRYHRYHGRSAAVWSLGILLYDMVCGDIPFEHDEEI-----VKGQVY-FRQRVSSEC
                                                                                                                                                                                                                                        ILRLFM--HPHIIRQYEVIETTSDIYVVMEYVKS-GELFDYIVEKGRLQEDEARNFFQQI
                                                                                                                                                                                                                                                                                                                        ESILPNYKLGKTLGIGSFGKVKIAEHVVTGHKVAIKILNRRKIKN---MEMEEKVRREIK
                                                                                                                                                                                                                                                                                                                                                            EPLESQYQVGPLLGSGGFGSVYSGIRVADNLPVAIKHVEKDRISDWGELPNGTRVPMEVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LSLRPSDRPSFEEIQNHPWMQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RYHGRSAAVWSLGILLYDMVCGDIPFEHD-----EEIVKGQVYFRQRVSSECQHLIRWC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CHSHHIVHRDLKTENLLLDANM-NIKLADFGFGNFYKSGEPLSTWCGSPPYAAPEVFEGK 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        --HPHIKLYQVMETKDMLYIVTEFAKN-GEMFDHLTSNGHLSESEARKKFWQILSAVEY 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SGFSGVIRLLDWFERPDSFVLILERPEPVQDLFDFITERGALQBELARSFFWQVLEAVRH
                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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C;Species: Xenopus laevis (African clawed frog)
C;Date: 07-May-1995 #sequence_revision 03-Aug-1995 #text_change 05-Oct-2004
C;Accession: S52244
R;Roghi, C:; le Guellec, R.; Paris, J.; Couturier, A.; Philippe, M.
submitted to the EMBL Data Library, October 1992
A;Description: Eg3, selected by differential screening encodes a new Xenopus protein kin A;Reference number: S5243
A;Reference number: S52243
A;Rocession: S52244
A;Kolecule type: mENA
A;Rocession: S52343
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Search completed: May 4, 2006, 05:25:52 Job time : 21.3333 secs
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NUCLEOTIDE SEQUENCE.

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Fujino Y., Satoh H., Hisasue M., Masuda K., Ohno K., Tsu
Fuh. acquence of the felline pim-1 oncogene.

I CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosph
II CATALYTIC ACTIVITY: ATP + a protein duclear (By similarity).

I SUBCELLULAR LOCATION: Cyroplasmic and nuclear (By si
II PTM: Autophosphorylated (By similarity).

I SIMILARITY: Belongs to the Ser/Thr protein kinase fa
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                                    Domen J., von Linde
Berns A.;
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Oncogene R
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MEDLINE-90382681; PubMed=2205533; D
Reeves R., Spies G.A., Kiefer M., B
"Primary structure of the putative
Gene 90:303-307(1990).
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P11309; Q96RG3;
O1-JUL-1989 (Rel. 11, Created)
O1-JAN-1990 (Rel. 13, Last seq
13-SEP-2005 (Rel. 48, Last ann
                                                                                                               NUCLEOTIDE SEQUENCE.

MEDLINE=87277423; PubMed=3475233; DOI=10.1016/0378-1119(87)90352-0;
Zakut-Houri R., Hazum S., Givol D., Telerman A.;
Telerman A.;
"The cDNA sequence and gene analysis of the human pim oncogene.";
Gene 54:105-111(1987).
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13-SEP-2005 (Rel. 48, Last annotation update)
Proto-oncogene serine/threonine-protein kinase
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Domen J., von Lindern
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3217305; PubMed=3329709;
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4; Mismatches
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ATP (By similarity).
                                                                                                                                                                                         DOI=10.1016/0378-1119(90)90195-W;
Barr P.J., Power M.;
e human oncogene, pim-1.";
                                                                      Α.,
                                      PIM-1 cDNAs: nucleotide sequence f the in vitro synthesized PIM-1
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RX MEDLINE-2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G. M., Hong L.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Raha S.S., Worley K.C., Hale S., García A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., García A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., García A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Wadan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Halbey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Halkesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
"Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sectuences.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pasqualucci L., Neumeister P., Goossens T., Nanjangud G., Chaganti R.S.K., Kuppers R., Dalla-favera R.; "Hypermutation of multiple proto-oncogenes in B-cell diffuetil lymphomas.";
Nature 412:341-346(2001).
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"Cloning
oncogene
                                                                                                                                                                                  "Pim-1 protein kinase is nuclear in Burkitt's lymphoma: nuclear localization is necessary for its biologic effects."; Anticancer Res. 23:167-178(2003).

-i- FUNCTION: Thought to play a role in signal transduction in cells. May affect the structure or silencing of chromatin b phosphorylating HP1 gamma/CBX3.

-i- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotei - SUBUNIT: Binds to RP9 (By similarity).

-i- SUBCELLULAR LOCATION: Cytoplasmic and nuclear.
-i- TISSUE SPECIFICITY: Expressed primarily in cells of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=20130009; PubMed=10664448; DOI=
Koike N., Maita H., Taira T., Ariga H.,
"Identification of heterochromatin prot
phosphorylation target by Pim-1 kinase
phosphorylation on the transcriptional
FEBS Lett. 467:17-21(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=22567470; PubMed=12680209; Ionov Y., Le X., Tunquist B.J., Sweetenham Johnson T., Lilly M.B., Kraft A.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Telerman A., Amson R., Zakut-Houri R., Givol D.;
"Identification of the human pim-1 gene product as a
cytoplasmic protein with tyrosine kinase activity.";
Mol. Cell. Biol. 8:1498-1503(1988).
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Meeker T.C., Nagarajan L., Ar-Rus
subfamily.
DATABASE: NAME=Atlas Genet.
WWW="http://www.infobiogen.
                                                                                               hematopoietic and germ line
PTM: Autophosphorylated on
SIMILARITY: Belongs to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mouse cDNA sequences."
c. Natl. Acad. Sci. U.S
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and characterization of the human
related to the protein kinases.";
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354098; PubMed=11460166;
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                                                                                                                                                                     line lineages.
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Ser/Thr p
         . Cytogenet. Oncol. Haematol.;
.fr/services/chromcancer/Genes/PIM1ID261.html".
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a H., Iguchi-Ariga S.M.M.;
protein I (HPI) as a
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EMBL; M16750; AAA60089.1; -; mRNA.
EMBL; M24915; AAA60089.1; -; mRNA.
EMBL; M24915; AAA36477.1; -; mRNA.
EMBL; M24779; AAA81153.1; -; mRNA.
EMBL; M24779; AAA81153.1; -; mRNA.
EMBL; BC020224; AAH20224.1; -; mRNA.
EMBL; BC020224; AAH20224.1; -; mRNA.
EMBL; JU0327; TVHUP1.

PDB; JXQZ; X-ray; A=14-313.
PDB; JXR1; X-ray; A=14-313.
PDB; JXR1; X-ray; A=13-31.
PDB; JYHS; X-ray; A=3-305.
PDB; JYHS; X-ray; A=3-305.
PDB; JYH4; X-ray; A=3-305.
PDB; JYH4; X-ray; A=3-305.
PDB; JYH4; X-ray; A=3-305.
PDB; JYH4; X-ray; B=1-313.
PDB; JEJL; X-ray; B=1-313.
PDB; JEJL; X-ray; B=1-313.
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DOMAIN
BOMAIN
BIND
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52
ACT SITE 167
BINDING
67
67
CONFLICT
15
5EQUENCE
313 AA; 35686
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MIM; 1649
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               888
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ensembl; ENSG0000
HGNC; HGNC:8986;
                                                                                                                                                                                                                                                                                                                                                                                                            3D-structure; ATP-binding; himase, nucleo-oncogene;
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30; GO:0005737; C:cytoplasm; TAS.
30; GO:0004674; F:protein serine/threonine kinase activity
30; GO:0004674; F:protein serine/TAS.
GO: GO:0007275; P:development; TAS.
GO: GO:0006468; P:protein amino acid phosphorylation; TAS.
InterPro; IPR0080719; Prot kinase.
InterPro; IPR008071; Ser Thr_pkin_AS.
              301
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                                                                                    EIHLHSLSPSPSK
                                     ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG
                                                                                                                                                                                                  NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL
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97.1%;
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ATP (By similarity).
Proton acceptor (By s
ATP (By similarity).
AP -> RA (in Ref. 2).
AP -> RA (in Ref. 2).
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Pred. No. 7.4e
6; Mismatches
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7.4e-113;
les 3;
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301

EIHLHSLSPGPSK

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EMBL; AL3535/9; Crand Sapiens.

DR SMR; Q5T7H7; 32-308.

EMBembl; ENSG00000137193; Homo sapiens.

DR GO; GO:0005524; F:ATP binding; IEA.

GO; GO:0005524; F:Protein serine/threonine kinase activity; IEA.

DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.

DR GO; GO:00046713; F:protein amino acid phosphorylation; IEA.

DR InterPro; IPR00121; Protein amino acid phosphorylation; IEA.

InterPro; IPR001271; Ser_thr_pkin_AS.

InterPro; IPR001271; Ser_thr_pkin_ase.

DR InterPro; IPR001245; Tyr_pkinase.

Pfam; PF00069; Pkinase; 1.

DR SMART; SM00219; TyrKc; 1.

DR SMART; SM00219; TyrKc; 1.

DR SMART; SM00219; PROTEIN_KINASE_ATP; 1.

DR PROSITE; PS00107; PROTEIN_KINASE_ST; 1.

ENCOSITE; PS00101; PROTEIN_KINASE_ST; 1.

KW ATP-binding; Kinase; Nucleotide-binding;

KW Serine/threonine-protein kinase; Transferase.

SMART; SM0213; TyrKc; 1.

KW Serine/threonine-protein kinase; Transferase.

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Eukaryota; Metazoa; C
Mammalia; Eutheria; E
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01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
Fim-1 oncogene (Proviral integration site 1).
Name=PIM1; ORFNames=RP3-355M6.1-003;
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OST7H7;
OST7H7;
O1-FEB-2005 (TrEMBLrel. 2)
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                                                                       ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG
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97.1%;
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7.4e-113;
hes 3;
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Matches 304;
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HSSP; Q63450; 1A06.
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Q9N0F9;
28-FEB-2003
28-FEB-2003
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SEQUENCE
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MEDLINE-21109090; PubMed=11182156; DOI=10.1016/S0165-2427(00)00259-2;

Mang Z., Petersen K., Weaver M.S., Magnuson N.S.;

"CDNA cloning, sequencing and characterization of bovine pim-1.";

Vet. Immunol. Immunopathol. 78:177-195(2001).

-I- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.

-I- SUBUNIT: Binds to RP9 (By similarity).

-I- SUBCILULAR LOCATION: Cytoplasmic and nuclear (By similarity).

-I- SUBCELTULAR LOCATION: Cytoplasmic and nuclear (By similarity).

-I- SUBCELTULAR LOCATION: Cytoplasmic and nuclear (By similarity).
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Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla;
Pecora; Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ProDom; PD000001; Prot_kinase; 1.
PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
ATP-binding; Kinase; Nuclear proTein; Nucleotide-binding; Phosphorylation; Proto-oncogene; Serine/threonine-protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9913;
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28-FEB-2003 (Rel. 41, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
Proto-oncogene serine/threonine-protein kinase
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InterPro; IPR008271; Ser_thr_pkin_AS.
Pfam; PF00069; Pkinase; I.
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                                                                                                                                                                             ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG
PFEHDEEIVKGQVYFRQRVSSECQHLIRWCLSLRPSDRPSFEEIQNHPWMQDVLLPQATA
                                                                                                                                                   ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHDCGVLHRDIKDENILIDLNRG
                                                                                                                                                                                                                                                   NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL
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nilarity 97.1%;
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52 A.
167 P.
67 A.
35630 MW;
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Pred. No. 2.1e-11
6; Mismatches
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ATP (By similarity).
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RC STRAIN=C57BL/6; TISSUE=Brain, and Eye;

RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RX AL STRAIN=C57BL/6; TISSUE=Brain, Arguer L. H., Derge J.G.,

RX AL Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RX AL Strausberg R.D., Collins F.S., Wagner L. Shenmen C.M., Schuler G.D.,

RX AL Stapender R.D., Collins F.S., Wagner L.M., Schaefer C.F., Bhat N.K.,

RX AL Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RX AL Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RX AL Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RX AL Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RX AL Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RX AL Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RX ARA S.S., Loquellano N.A., Peters G.J., Abrameon R.D., Mullahy S.J.,

RX ARA S.S., Loquellano N.A., Peters G.J., Abrameon R.D., Mullahy S.J.,

RX ARA S.S., MocEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RX ARA S.S., MocTey K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RX ARA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RX ARA Whiting M., Madan A., Young A.C., Shevchenko Y., Boutfard G.G.,

RX ARA Whiting M., Madan A., Young A.C., Shevchenko Y., Boutfard G.G.,

RX ARA Bakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RX ARA Bakesley R.W., Touchman J.W., Schmutz J., Myers R.M.,

RX Ghmerch A., Schein J.E., Jones S.J.M., Marra M.A.;

"Generation and initial analysis of more than 15,000 full-length human

RX Tand mouse cDNA sequences ";

PARO MICH. Acad. Sci. U.S.A. 99:16899-16903 (2002).
Submitted (JUL-2003) to the EMBL/GenBank/DDBJ-!- CATALYTIC ACTIVITY: ATP + a protein = ADP-!- SIMILARITY: Belongs to the Ser/Thr protein EMBL; BC042885; AJH42885.1; -; mRNA. EMBL; BC042885; AJH42885.1; -; mRNA. EMBL; BC053019; AAH53019.1; -; mRNA. EMBL; BC055316; AAH53019.1; -; mRNA. EMBL; BC055316; AAH55316.1; -; mRNA. EMBL; BC05316; AAH55316.1; -; mRNA. EMBL; BC05316; AAH55316.1; -; mRNA. EMBL; BC05316; ENSWUSG0000024014; Mus musculus. SMR; OBCFN8; 7: PFATP binding; IEA. GO; GO:0004678; P:protein serine/threonine kingo; GO:0004648; P:protein amino acid phosphor. InterPro; IPR000719; Prot_kinase.
                                                                                                                                                                                                                                                                                                                                                                         NUCLEOTIDE SEQUENCE.
STRAIN=C57BL/6; TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=C57BL/6; TISSUE=Brain;
Strausberg R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q8CFN8_MOUSE
                                                                                                                                                                                                                                                                                                                                                      Strausberg R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted
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Eukaryota; Metazoa; Chordata; Craniato
Mammalia; Butheria; Euarchontoglires;
Muridae; Murinae; Mus.
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10-MAY-2005 (TrEMBLrel.
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Last annotation updat
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oglires; Glires;
                           eonine kinase activity; phosphorylation; IEA.
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protein kinase family.
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Best Local S
Matches 296
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InterPro; IPR002290; Ser_thr_pkinase.
Iffam; pr00060; pkinase; i.
ProDom; pD000001; prot_kinase; 1.
SMART; SM00220; S TKC; 1.
SMART; SM00220; S TKC; 1.
SMART; SM00220; S TKC; 1.
PROSITE; PS00107; PROTEIN_KINASE_DOM; 1.
PROSITE; pS00101; PROTEIN_KINASE_DOM; 1.
PROSITE; pS00108; PROTEIN_KINASE_T; 1.
PROSITE; PS00108; PROTEIN_KINASE_T; 1.
PROSITE; PS00108; PROTEIN_KINASE_T; 1.
SPROSITE; PS00108; PROTEIN_KINASE_TOM; 1.
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SPROSITE; PROTEIN_KINASE_TOM; 1.
SPROSITE; PROTEIN_
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MEDLINE=20389540; PubMed=10931201;
Maita H., Harada Y., Nagakubo D., Kitaura H., Iked
Takahashi K., Ariga H., Iguchi-Ariga S.M.M.;
"PAP-1, a novel target protein of phosphorylation
Eur. J. Biochem. 267:5168-5178(2000)
-!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a
-!- SUBUNIT: Binds to RP9.
                                                                                                                                                                                                                                                                  NUCLEOTIDE SEQUENCE.
MEDLINE=86272109; PubMed=3015420; DOI=1
Selten G., Cuypers H.T., Boelens W., Ro
Domen J., van Beveren C., Berns A.;
"The primary structure of the putative
homology with protein kinases.";
Cell 46:603-611(1986).
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Mammalia; Eutheria;
Muroidea; Muridae; N
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13-SEP-2005
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                                                                                                                                                                                                                   INTERACTION WITH RP9.
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V., Robanus-Maandag E., Verbeek J.
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RESULT 8

PIM3_COTJA

ID PIM5_COTJA STANDARD; PRT; 323 AA.

AC Q9PUB5;

DT 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2005 (Rel. 41, Last sequence update)

DT 13-SEP-2005 (Rel. 48, Last annotation update)

DT 13-SEP-2005 (Rel. 48, Last annotation update)

DE Serine/threonine-protein kinase Pim-3 (EC 2.7.1.37)

GN Name=PIM3; Synonyms=PIM-3;

GS Coturnix coturnix japonica (Japanese quail).
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HSSP; Q63450; 1A06.
SMR; P06803; 32-308.
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MGI; MGI:97584; Piml.

InterPro; IPR000719; Prot_kinase.

InterPro; IPR000871; Ser_thr_pkin_AS.

Pfam; PP00069; Pkinase; I.

ProDom; PD000001; Prot_kinase; 1.

PROSITE; PS00107; PROTEIN KINASE_ATP; 1.

PROSITE; PS00108; PROTEIN KINASE_DOM; 1.

PROSITE; PS001108; PROTEIN KINASE_ST; 1.

ATP-binding; Kinase; Nuclear protein; Nucleotide-binding;

ATP-binding; Kinase; Nuclear protein; Nucleotide-binding;
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PIR; A24169; TVMSP1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1
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-I- CATALYTIC ACTIVITY; ATP + a protein = ADP + a phosphoprotein -: PTW: Autophosphorylated.
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NP_BIND
ACT_SITE
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SMART; SM00120; S.TKC; 1.

PROSITE; PS00107; PROTEIN KINASE_ATP; 1.

PROSITE; PS50011; PROTEIN KINASE_DOM; 1.

PROSITE; PS00108; PROTEIN_KINASE_ST; 1.

ATP-binding; Kinase; Nucleotide-binding; Phosphorylation;
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InterPro; IPR000719; Prot kinase.
InterPro; IPR008271; Ser_thr_pkinase.
InterPro; IPR008290; Ser_thr_pkinase.
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                                                                                                                                                                                                                                                                                                           54 A
168 P
69 A
36597 MW;
                                                                                                                                                                                                                                                                            68.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    content is
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Neognathae; Galliformes; Phasianidae; Phasiani
                     312
                                                                                                                                                                                                                                                                   43;
                                                                                                                                                                                                                                                                 Score 1137; DB 1;
Pred. No. 6.2e-76;
3; Mismatches 56;
                                                                                                                                                                                                                                                                                                           Protein kinase.
ATP (By similarity).
Proton acceptor (By similarity).
ATP (By similarity).
; E2A4FA20B6F6396C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    in no
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                                                                                                                                                                                                                                                                                       Length
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                                                                                       LGALTADWACC
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                                                                                                                                   179
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                                                                 297
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RESULT 9
PIM3\_HUMAN
ID PIM3\_HUMAN

STANDARD;

PRT;

326 AA

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RA Strausberg R.L., Feungold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Ra Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Stapleton M., Godin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Ra Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunarathe P.H.,
RA Hibrards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Villalon D.K., Wong A.C., Shevchenko Y., Bouffard G.G.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Rodriguez A.C., Grinwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalaka U., Smailus D.E.,
"Generation and initial analysis of more than 15,000 full-length human
"Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HGNC; HGNC:19310; PIM3.
HGNC; HGNC:19310; Prot kinase.
InterPro; IPR008271; Ser_Ehr_pkin_AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hepatocellular carcinoma development of human hepatoma cell lines."; Int. J. Cancer 114:209-218(2005).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=22388257;
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Mammalia; Eutheria;
                                                                                                                             Ensembl;
                                                                                                                                                          EMBL; AB114795; BAD42438.1; EMBL; BC052239; -; NOT_ANNO
                                                                                                                                                                                                                                                                                                                                                                                                       This
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fujii
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9606
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Serine/threonine-protein kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29-MAR-2004 (Rel.
13-SEP-2005 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q86V86; Q68BM2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kaneko S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                         apoptosis process. Implicateu 1... - apoptosis process. Implicateu 1... - cell lines.

CATALYTIC ACTIVITY: ATP + a protein = ADP + a |
TISSUE SPECIFICITY: Widely expressed. No exprethymus, and small intestine. Expressed in humalines but not in normal liver tissues.

THE CONTROL OF THE CONTR
                                                                                                                                                                                                                                                                                                                           s Swiss-Prot entry is copyright. It is produced ween the Swiss Institute of Bioinformatics and European Bioinformatics Institute. There are r
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mouse cDNA sequences.";
c. Natl. Acad. Sci. U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C., Nakamoto
                                                                                                                                                                                                                                                                                              Puor
                                                                                                                  052239; -; NOT ANI
ENSG00000198355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE [LARGE SCALE MRNA]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mukaida N.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   [MRNA],
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Last sequence update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99:16899-16903 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tsuneyama
                                                                                                                      sapiens
                                                                                                                                                                                          mRNA
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i J.-C., Lisacek F.;
zing protein forms.";
                                                                                                                                                                                                                                                                                              way
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(EC 2.7
                                                                                                                                                          mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SPECIFICITY
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REPRESENTATION OF THE PROPERTY OF THE PROPERTY

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DR PROSTTE; PS00101; PROTEIN_KINASE, 1.

DR PROSTTE; PS00101; PROTEIN_KINASE ATP; 1.

DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.

DR PROSITE; PS00108; PROTEIN_KINASE_TOM; 1.

KW ATP-binding; Kinase; Nuclectide-binding; Phosphorylation; Serine/threonine-protein kinase; Transferase.

KW Serine/threonine-protein kinase; Transferase.

FT DOMAIN 40 293 Protein kinase.

FT NPBIND 46 54 ATP (By similarity).

FT ACT_SITE 170 170 Proton acceptor (B. Tenton) acceptor (B. Tent
          В
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RC STRAIN=FVB/N, TISSUE=Colon, and Salivary gland;

RX MEDLINE=22388257; PubMed=124779312; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Alusner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetcw K.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Jordan H., Moore T., Max S.I., Wang L.,

RA Hopkins R.F., Jordan H., Moore T., Max. S.I., Wang L.,

RA Hopkins R.F., Jordan H., Moore T., Max. S.I., Wang L.,

RA Diatchenko L., Warusina K., Farmer A.A., Rubin G.M., Hong L.,

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RA Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Hichards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Willalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
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Best Local S
Matches 220
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Mammalia; Eutheria; Euarchontoglires;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Serine/threonine-protein
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13-SEP-2005
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Muroidea; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Name=Pim3;
                                                                                                                                                                                                                                                                                                                                                                                                   NUCLEOTIDE SEQUENCE [LARGE SCALE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VADNLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKV--SSGFSGVIRLLDWFBRPDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VCGDIPFEQDEEILRGRLLFRRRVSPECQQLIRWCLSLRPSERPSLDQIAAHPWMLGADG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VCGDIPFEHDEEIVKGQVYFRQRVSSECQHLIRWCLSLRPSDRPSFEEIQNHPWM--QDV
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(Rel. 41,
(Rel. 48,
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Last annotation
ein kinase Pim-3
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Pred. No. 8.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 update)
(EC 2.7.1.37).
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RESULT 11
PIM3_RAT
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Best Local :
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ProDom; PD000001; Frot kinase; 1.

SMART; SM00220; S TKc; 1.

PROSITE; PS00107; PROTEIN KINASE DOM; 1.

PROSITE; PS00108; PROTEIN KINASE ST; 1.

PROSITE; PS00108; PROTEIN KINASE ST; 1.

ATP-binding; Kinase; Nucleotide-binding; Phosphorylation;

Thronine-protein kinase; Transferase.
PIM3_RAT STANDARD; PRT; 326 AA.

070444;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
Serine/threonine-protein kinase Pim-3 (EC 2.7.1.37)
Kid-1) (Kinase induced by depolarization).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN

NP BIND

ACT SITE

BINDING

SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length hand mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
--- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
--- SIMILARITY: Belongs to the Ser/Thr protein kinase family. PIM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MGI; MGI:1355297; Pim3.
InterPro; IPR008721; Ser thr pkin
InterPro; IPR008271; Ser thr pkin
InterPro; IPR002290; Ser thr pkin
Pfam; PF00069; Pkinase; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; BC017621; AAH17621.1;
EMBL; BC026639; AAH26639.1;
HSSP; Q03656; 1HOW.
Ensembl; ENSMUSG00000035828
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                s Swiss-Prot entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the EN European Bioinformatics Institute. There are no rest as long as its content is in no way modified and this a
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214; Conserv
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                                                                                                                                                   VCGDIPFEQDEEILRGRLFFRRRVSPECQQLIEWCLSLRPSERPSLDQIAAHPWM
                                                                                                                                                                              VCGDI
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170
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326 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein kinase.
ATP (By similarity).
Proton acceptor (By similarity)
ATP (By similarity).
pdb8CBF46354851E CRC64;
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Pred. No. 1.3e-7
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Best Local S
Matches 214
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EMBL; AF057026; AAC36065.1; -; mRNA.

HSSP; Q03656; 1HOW.

RGD; 620462; Pim3.

GO; GO:0004674; F:protein serine/threonine kinase act
GO; GO:0016777; P:autophosphorylation; IDA.
GO; GO:0016572; P:histone phosphorylation; IDA.
GO; GO:0016572; P:histone phosphorylation; IDA.
InterPro; IPR008271; Ser Chr pkin_AS.
InterPro; IPR008271; Ser Chr pkin_AS.
InterPro; IPR008270; Ser Thr_pkinase.
                                                                                                                                                                                                                                                 ACT SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUCLEOTIDE SEQUENCE, AND CHARACTERIZATION.

MEDLINE=98298176; PubMed=9632723; DOI=10.1074/jbc.273.26.16535;

Feldman J.D., Vician L., Crispino M., Tocco G., Marcheselli V.L.,

Bazan N.G., Baudry M., Herschman H.R.;

Bazan N.G., Brudry M., Herschman H.R.;

"KID-1, a protein kinase induced by depolarization in brain.";

"KID-1, a protein kinase induced by depolarization in brain.";

J. Biol. Chem. 273:16535-16543 (1998).

-i- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.

-i- TISSUE SPECIFICITY: Present in a number of unstimulated tissu
                                                                                                                                                                                                                                                                                                                         ProDom; PD000001; Prot kinase; 1.

SMART; SM00220; S TKC; 1.

PROSITE; PS00107; PROTEIN KINASE ATP; 1.

PROSITE; PS50011; PROTEIN KINASE DOM; 1.

PROSITE; PS00108; PROTEIN KINASE ST; 1.

PROSITE; PS00108; PROTEIN KINASE ST; 1.

ATP-binding; Kinase; Nucleotide-binding; Phosphorylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-Sprague-Dawley;
Konietzko U., Kuhl D.;
"Pim-3 is a member of the pim kinase family.";
Submitted (AUG-1998) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rattus norveĝicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                including brain.
-!- INDUCTION: By membrane depolarization
-!- PTM: Autophosphorylated.
-!- SIMILARITY: Belongs to the Ser/Thr pro
                                                                                                                                                                                                                                                                                                             Serine/threonine-protein
                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00069; Pkinase;
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                                                                                                                                                                                                                                                                                               DOMAIN
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                                                     MLLSKFGSLAHL-CGPGGVDHLPVKILQPAKADKESFEKVYQVGAVLGSGGFGTVYAGSR
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FLLVLERPEPAQDLFDFITERGALDEPLARRFFAQVLAAVRHCHNCGVVHRDIKDENLLV
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ATP (By similarity).
Proton acceptor (By similarity).
ATP (By similarity).
                                                                                                                                                                           Score 1131.5; DB
Pred. No. 1.6e-75;
0; Mismatches 44
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rfam; pro0069; Pkinase; 1.

R proDom; pr000001; Prot kinase; 1.

R SMART; SM00220; S_TKC; 1.

R SMART; SM00220; TyrKC; 1.

R PROSITE; PS00107; PROTEIN KINASE_DOM; 1.

DR PROSITE; PS00101; PROTEIN_KINASE_DOM; 1.

DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.

PROSITE; PS00108; PROTEIN_KINASE_ST; Nuclective ATP-binding; Hypothetical protein; Kinase; Nuclective ATP-binding; Hypothetical protein kinase; Transferase.
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RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
RA Altechul S.F., Zeeberg B., Buecow K.H., Schaefer C.F., Bhat N.K.,
RA Altechul S.F., Zeeberg B., Buecow K.H., Schaefer C.F., Bhat N.K.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Rahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Rahey J., Hall M., Sodergren E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
"Generation and initial analysis of more than 15,000 full-length human and mouse cDNA secunences ""
"Generation and initial analysis of more than 15,000 full-length human
  Query Match
Best Local S
Matches 214
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Q4V8M2;
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SEQUENCE
                                                                                                                                                                                                                                                                                                           Submitted (JUN-2005) to the EMBL/GenB.
-:- SIMILARITY: Belongs to the Ser/Th.
EMBL; BC097317; AAH97317.1; -; mRNA.
InterPro; IPR000719; Prot kinase.
InterPro; IPR0002719; Ser_thr_pkin_AS.
InterPro; IPR002290; Ser_thr_pkinase.
InterPro; IPR001245; Tyr_pkinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertel
Mammalia; Eutheria; Euarchontoglires; Glires;
Muroidea; Muridae; Murinae; Rattus.
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    Local Similarity
mes 214; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mouse cDNA sequences.";
c. Natl. Acad. Sci. U.S.A.
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                     67.8%;
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                     Score 1131.5;
Pred. No. 1.96
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                                                                                  F82BE8E50DD71346
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lires; Rodentia; Sciurognathi;
                     9e-1
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                                       DB 2;
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n kinase family.
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01-JUN-2003
01-MAR-2004
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Q811X8 MOUSE
Q811X8;
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R HSSP; Q03656; 1403.

R SMR; Q811X8; 36-292.

DR MGI; MGI:1355297; pim3.

DR GO; GO:0005524; F:ATP binding; IEA.

GO; GO:0005524; F:Protein serine/threonine kinase activity

GO; GO:0004674; F:protein amino acid phosphorylation; IEA

DR GO; GO:0004678; P:protein amino acid phosphorylation; IEA

InterPro; IPR000719; Prott kinase.

DR InterPro; IPR000719; Ser thr_pkin_AS.

Pfam; PF00069; Pkinase; I.

DR ProDom; PD000001; Prott kinase; 1.

DR PROSITE; PS00107; PROTEIN_KINASE_DOM; 1.

DR PROSITE; PS00107; PROTEIN_KINASE_DOM; 1.

DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.

TROM ATP-binding; Kinase; Nucleotide-binding;

Serine/threonine-protein kinase; Transferase.

Serine/threonine-protein kinase; Transferase.
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EMBL; AY026239; AAK16606.1; -; mRNA.
HSSP; Q03656; 1Q99.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Name=Pim3; Synonyms=Kid1;
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=10090;
 119
                                                                                                                                                                                                         al Similarity
213; Conserv
MLLSKINSLAHLRAAP--CNDLHANKLAPGK-EKEPLESQYQVGPLLGSGGFGSVYSGIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Murinae;
                                                                                      VADNLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKV--SSGFSGVIRLLDWFERPDS
                                                                                                                                       MLLSKFGSLAHL-CGPGGVDHLPVKILQPAKADKESFEKVYQVGAVLGSGGFGTVYAGSR
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                                                                                                                                                                                                         Conservative
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                                                                                                                                                                                                                                          Score
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-GGVAVPLEVVLLRKVGAAGGARG
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RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschenko L., Marusina K., Farmer A.A., Rubin G.M., Hsieh F.R.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
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RA Raha S.S., Loguellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Raha S.S., Loguellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
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RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Whilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Butterfield Y.S.N., Krzywinski M.I., Schmers R.M.,
ROdriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
"Generation and initial analysis of more than 15,000 full-length human
"Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
                                                                                                                                                                                                  GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0004674; F:protein serine/threonine kinase activity;
GO; GO:0004673; F:protein-tyrosine kinase activity; IEA.
GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
InterPro; IPR000719; Prot kinase.
InterPro; IPR008271; Ser_thr_pkin_AS.
InterPro; IPR008279; Ser_thr_pkinase.
InterPro; IPR001245; Tyr_pkinase.
InterPro; IPR001245; Tyr_pkinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   066111
                                                                                     ProDom; PD000001; Prot_kinase; 1.
SMART; SM00220; S_TKC; 1.
SMART; SM00219; TyrKC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899; Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Xenopus tropicalis (Western clawed frog) (Silurana tropicalis).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q66111
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                                                                                                                                                                                        Pfam; PF00069; Pkinase;
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PS00107; PROTEIN_KINASE_ATP; 1.
PS50011; PROTEIN_KINASE_DOM; 1.
PS00108; PROTEIN_KINASE_ST; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VCGDIPFEHDEEIVKGQVYFRQRVSSECQHLIRWCLSLRPSDRPSFEEIQNHPWM
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RESULT 15
PIM3_XENL
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Best Local S
Matches 205
               EMBL; L29495; AAA85389.1; mRNA.
InterPro; IPR000719; Prot kinase.
InterPro; IPR008271; Ser Thr pkin_AS.
Pfam; PF00069; Pkinase; 1.
ProDom; PD000001; Prot kinase; 1.
PROSITE; PS00107; PROTEIN KINASE DOM; PROSITE; PS00119; PROTEIN KINASE TOP; 1
PROSITE; PS00108; PROTEIN_KINASE_ST; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PIM3 XENLA STANDARD; PRT; 323 AA 091822; 15-DEC-1998 (Rel. 37, Created) 15-DEC-1998 (Rel. 37, Last sequence update) 13-SEP-2005 (Rel. 48, Last annotation updat Serine/threonine-protein kinase Pim-3 (EC 2
                                                                                                                                                                                                                                                                                                            Pim-1 proto-oncogene-encoded protein kinase.",
J. Biol. Chem. 272:10514-10521(1997).
-i- CATALYTIC ACTIVITY: ATP + a protein = ADP
                                                                                                                                                                                                                                                                                                                                                                     NUCLEOTIDE SEQUENCE, AND PHOSPHORYLATION SITES.
MEDLINE=97256766; PubMed=9099695; DOI=10.1074/jbc.272.16.10514;
Palaty C.K., Kalmar G., Tai G., Oh S., Amankawa L., Affolter M.,
Aebersold R., Pelech S.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            XENLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATP-binding; Cell cycle; Cell division; Kinase; Nucleotide-binding; Serine/threonine-protein kinase; Transferase.
SEQUENCE 318 AA; 36547 MW; 48CCF12797F01FDC CRC64;
                                                                                                                                                                             This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Ver
Amphibia; Batrachia; Anura; Mesobatrachia;
Xenopodinae; Xenopus; Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Name=PIM3; Synonyms=PIM1;
                                                                                                                                                                   use as
                                                                                                                                                                                                                                                                                                                                                        "Identification of the autophosphorylation sites of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kenopus laevis (African clawed
                                                                                                                                                    cemoved.
                                                                                                                                                                                                                                   subfamily.

CAUTION: Was originally (Ref.1) called represent the pim-3 isoform.
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Prot kinase; 1.

PROTEIN KINASE ATP; FALSE NEG.

PROTEIN_KINASE_DOM; 1.

PROTEIN_KINASE_ST; 1.

se; Nucleotide-binding; Phosphorylation;
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Pred. No. 5.5e
40; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Craniata; Vertebrata;
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(EC 2.7.1.37)
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Search completed: May Job time : 123 secs	236 1		175 I	116 /	115 8	57 E	55 0	μ 7	1 - 3	Query Match Best Local Similarity Matches 203; Conser	SEQUENCE	MOD_RES	MOD_RES	MOD_RES	BINDING	ACT SITE	DOMAIN	Serine/threonine-protein
	VYGDIPFE(		DLNRGELKI	FLIVMER PI	FVLILERPI	SRIADGQP	BIRVADNLP	MLLSKFGSLAHI	TEKINSL	66. il Similarity 68. 203; Conservative	323 AA;	205	190	4.	69	168	40	eonine-p
4, 2006,	DEEIVRVR		LIDFGSGAL	EPVKDLFDY	EPVODLEDE	VAVKHVAKE	VAIKHVEKD	AHICN	AHLRAAPCN	* * 6 H	36964 MW;	205	190	4.	69	168	291	rotein ki
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2: /cgn2_6/ptodata/1/iaa/6_COMB.pep:*

3: /cgn2_6/ptodata/1/iaa/H_COMB.pep:*

4: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

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Sequence 7, Application US/09237543A
Patent No. 6143540
GENERAL INFORMATION:
APPLICANT: KABCHIET, ROSANA
TITLE OF INVENTION: NOVEL MOLECULES OF THE HK
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: 03500/175631
CURRENT APPLICATION NUMBER: US/09/237,543A
CURRENT FILING DATE: 1999-01-26
NUMBER OF SEQ ID NOS: 11
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 7
LENGTH: 313
TYPE: PAT
ORGANISM: Mus musculus
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APPLICANT: Kapeller, Rosana
ITTLE OF INVENTION: NOVEL MOLECULES OF THE
ITTLE OF INVENTION: AND USES THEREOF
ITLE OF INVENTION: AND USES THEREOF
ITLE REFERENCE: 035800/175631
CURRENT APPLICATION NUMBER: US/09/644,450
CURRENT APPLICATION OUMBER: US/09/644,450
CURRENT FILING DATE: 2000-08-23
NUMBER OF SEO ID NOS: 11
SOFTMARE: Patentin Ver. 2.0
SEO ID NO 7
SEO ID NO 7
LENGTH: 313
TYPE: PRT
ORGANISM: Mus musculus
US-09-644-450-7
                                                                                                                                            Sequence 8, Application US/09237543A

Patent No. 6143540

GENERAL INFORMATION:
APPLICANT: Kapellar, Rosana
TITLE OF INVENTION: NOVEL MOLECULES OF THE HK
TUTLE OF INVENTION: NOVEL MOLECULES OF THE HK
TUTLE OF INVENTION: 1999-01-26

NUMBER OF SEQ ID NOS: 11
SOFTMARE: PATENTIN Ver. 2.0
SEQ ID NO 8
LENGTH: 313
TYPE: PRT
ORGANISM: Rattus norvegicus
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APPLICANT: Kapeller, Rosana
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Patent No. 638791
GENERAL INFORMATION:
APPLICANT: Kapeller, Rogana
ITILE OF INVENTION: NOVEL MOLECULES OF THE
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: 035800/175631
CURRENT APPLICATION NUMBER: US/09/644,450
CURRENT FILING DATE: 2000-08-23
NUMBER OF SEQ ID NOS: 11
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 8
LENGTH: 313
TYPE: PRT
ROGANISM: Rattus norvegicus
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Sequence 9, Application US/09237543A Patent No. 6143540
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ilarity 94.2%;
Conservative (
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Pred. No. 3.4e-153;
8; Mismatches 10;
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APPLICANT: Kapeller, Rosana
TITLE OF INVENTION: NOVEL MOLECULES OF THE
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: 035800/175631
CURRENT APPLICATION NUMBER: US/09/644,450
CURRENT FILING DATE: 2000-08-23
NUMBER OF SEQ ID NOS: 11
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 9
LENGTH: 313
TYPE: PAT
ORGANISM: Homo sapiens
US-09-644-450-9
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TITLE OF INVENTION: NOVEL MOLECULES OF THE HKID-1-RELATED PROTEIN FAMILY
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: 035800/175631
CURRENT APPLICATION NUMBER: US/09/237,543A
CURRENT FILING DATE: 1999-01-26
NUMBER OF SEQ ID NOS: 11
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 9
LENGTH: 313
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Best Local Similarity
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ilarity 93.9%;
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93.9%; Pred. No. 5.4e-153;
tive 10; Mismatches 9;
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Pred. No. 5.4e-153;
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RESULT 7
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US-08-463-081B-26
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                                                                                                  APPLICATION NUMBER: US 07/796,066
FILING DATE: 20-NOV-91
ATTORNEY/AGENT INFORMATION:
NAME: Viviana Amzel, Ph. D.
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: P66 38150 (
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 622-7700
TELEPHONE: (213) 622-7700
TELEPHONE: (213) 489-4210
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 313 amino acids
TYPE: amino acids
STRANDEDNESS: n.a.
TOPOLOGY: n.a.
 Query Match
Best Local S
Matches 294
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 08/104,736 FILING DATE: 10-AUG-1993 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Smith, Kendall A. & Beadling, TITLE OF INVENTION: Nucleic Acids Encodir TITLE OF INVENTION: Vector and Transforme NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/
FILING DATE: 5-JUN-1995
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 444 South
CITY: Los Angeles
STATE: California
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Application US/08463081B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          USA
94.7%; Score 1580; DB 1;
larity 93.9%; Pred. No. 8.6e-153;
Conservative 10; Mismatches 9;
                                                                                        peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and Transformed
                                                                                                                                                                                                                                                                        38150 (DART-060)
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Cell Thereof, and Expression
                                Length 313;
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RESULT 8
US-08-461-379A-26
; Sequence 26, App
                                                                             TOPOLOGY: n.;
MOLECULE TYPE:
US-08-461-379A-26
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                                                                                                                                                                                                                COMPUTER 19482

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PALENTION PT:

SOFTWARE: PALENTION DATA:

APPLICATION NUMBER: US/08/461,379A

FILING DATE: 5-UUNE-1995

PRIOR APPLICATION NUMBER: US/08/330,108; 08/104,736

APPLICATION NUMBER: W 07/796,066

FILING DATE: 27-OCT-1994; 10-AUG-1993 & 20-NOV-91

ATTORNEY/AGENT INFORMATION:

NAME: Viviana Amzel, Ph. D.

REFERENCE/DOCKET NUMBER: 30,930

REFERENCE/DOCKET NUMBER: 30,930

REFERENCE/DOCKET NUMBER: MET-070

TELECOMMUNICATION INFORMATION:

TELEPHONE: (610)470-0700
              Query Match
Best Local Similarity
Matches 294; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Patent No. 5871961
GENERAL INFORMATION:
                                                                                                                                                                                         TELEFAX: (610)470-0701
INFORMATION FOR SEQ ID NO: 26:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Smith, Kendall A. & Beadling, Carol TITLE OF INVENTION: Nucleic Acids Encoding CR5 Polypeptide, TITLE OF INVENTION: Vector and Transformed Cell Thereof, and TITLE OF INVENTION: Expression Thereof NUMBER OF SEQUENCES: 35

CORRESPONDENCE ADDRESS:
                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 313 amino acid
                                                                                                                         TYPE: peptide
STRANDEDNESS: n.a.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Valley Forge STATE: Pennsylvania COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Ratner & Prestia
ADDRESSEE: (B) STREET:One Westlakes-Berwyn
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5. 5871961
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                                                                                                                                                        313 amino acids
                  Conservative
                                                                                           peptide
                94.7%; Score 1580; DB 1;
93.9%; Pred. No. 8.6e-153;
93.9%; Pred. No. 8.6e-153;
                                             DB 1; Length 313;
                Indels
                  0
                  Gaps
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Query Match
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; MOLECULE TYPE: US-08-462-390B-26
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                                                                                                                                                TELEPAX: (610,70. 7
INFORMATION FOR SEQ ID NO: 7
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Smith, K. A., & Beadling, C.
TITLE OF INVENTION: Nucleic Acids Encoding CRB Polypeptide, Vector and
TITLE OF INVENTION: Transformed Cell Thereof, and Expression Thereof
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/462,390B
FILING DATE: 5-UNE-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/330,108
FILING DATE: USSN 08/330,108
FILING DATE: USSN 08/330,108
FILING DATE: USSN 08/30,108
APPLICATION NUMBER: USSN 08/04,736
FILING DATE: 10-AUG-1993
APPLICATION NUMBER: USSN 08/104,736
FILING DATE: 10-AUG-1993
APPLICATION NUMBER: USSN 07/796,066
                                                                                                                                                                                                                                                                   FILING DATE: 20-NOV-91
ATTORNAY/AGENT INFORMATION:
NAME: Viviana Amzel, Ph. D.
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: DART
TELECOMMUNICATION INFORMATION:
TELEPHONE: (610)407-0700
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STATE: Pennsylvania
                                                                                                TOPOLOGY:
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                                                                                                                       STRANDEDNESS:
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5. 5882894
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61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120
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                                                                                                                                                                                                                   (610) 407-0701
TD NO: 26:
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                                                                                                                                                                       amino acids
                                                                    peptide
                                                                                                                       n.a.
  94.7%;
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  Score 1580;
  В
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Length 313;
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US-08-463-074B-26
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GENERAL INFORMATION:
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                                                                                                                                                                                             APPLICATION NUMBER: US 07/796,066
FILLING DATE: 20-NOV-91
ATTORNEY/AGENT INFORMATION:
NAME: VIVIANA AMZel, Ph. D.
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: P66 38143
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 622-7700
                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
SOFTWARE: PatentIn Release #1.0,
SOFTWARE: Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/08/463,074B
FILING DATE: 5-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/104,736
FILING DATE: 10-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
                                                                                                                         TELEFAX: (213) 489-4210
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
                       TOPOLOGY: n
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION:
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CITY: Los
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                                                               STRANDEDNESS:
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0; Mismatches 9;
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Patent No. 6027914
GENERAL INFORMATION:
APPLICANT: Smith, K. A., & Beadling, C.
TITLE OF INVENTION: Nucleic Acids Encoding CR6
TITLE OF INVENTION: Transformed Cell Thereof, a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 94.7
Best Local Similarity 93.9
Matches 294; Conservative
                                                                                                  COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Versi
CURRENT APPLICATION NUMBER: US/08/465,585C
FILING DATE: 5-JUNE-1995
FRIOR APPLICATION NUMBER: USSN 08/330,108
FILING DATE: 27-OCT-1994
APPLICATION NUMBER: USSN 08/104,736
FILING DATE: 10-AUG-1993
APPLICATION NUMBER: USSN 07/796,066
FILING DATE: 10-AUG-1993
APPLICATION NUMBER: USSN 07/796,066
FILING DATE: 20-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: VLY1ana Amzel, Ph. D.
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: P66 38149 (DA
TELECOMMUNICATION INFORMATION:
                                                          TELEFAX: (213) 4894210 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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ZIP: 900071
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STATE: Californiaa
STRANDEDNESS
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                                       313 amino acids
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. (B) STREET:
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Patent No. 6057427
GENERAL INFORMATION:
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                                                   FILING DATE:

PRIOR APPLICATION DATA:
APPLICATION UNMBER: EP App. # 96921319
APPLICATION UNMBER: PCT/US/96/09194
FILING DATE: 5-JUN-1996
FILING DATE: 5-JUN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/330,108
FILING DATE: 27-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/463,074
PRIOR APPLICATION NUMBER: 08/463,074
                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Smith, Kendall A. & Beadling, Carol TITLE OF INVENTION: Nucleic Acids Encoding CR5
TITLE OF INVENTION: Polypeptide, Vector and Transformed Cell Thereof, and TITLE OF INVENTION: Expression Thereof
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
             FILING DATE: 5-JUN-1995 PRIOR APPLICATION DATA: APPLICATION NUMBER: 08/
                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
SOFTWARE: Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/652,44
                                                                                                                                                                                                                                                                                                                                 ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                CITY: Los Angeles
STATE: California
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93.9%; Pred. No. 8.6e-153;
tive 10; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                               SCHROEDER & POPLAWSKI
                                                                                                                                                                                   EP App. # 96921319.8
              08/462,337
                                                                                                                                                                                                                                      US/08/652,446
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                                                          Sequence 41, Application US/07857224B
Patent No. 5958784
GENERAL INFORMATION:
APPLICANT: Benner, Steven A.
TITLE OF INFORMATION: Predicting Fo.
NUMBER OF SEQUENCES: 114
CORRESPONDENCE ADDRESS:
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                            ADDRESSEE: Steven A. Benner
STREET: Hadlaubstrasse 151
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                Zurich
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none
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TOPOLOGY: n.a.;
MOLECULE TYPE: peptide
US-08-652-446-26
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Best Local Similarity
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INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
SEQUENCE 313 amino acids
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FILING DATE: 29-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Viviana Amzel, Ph. D.
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: FP66 40
TELECOMMUNICATION INFORMATION:
TELECHONE: (213) 622-7700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/46
FILING DATE: 5-JUN-1995
PRIOR APPLICATION NUMBER: 08/46
APPLICATION NUMBER: 08/46
FILING DATE: 5-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 08/
FILING DATE: 5-JUN-1991
PRIOR APPLICATION DATA:
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APPLICATION NUMBER: 08/463,081
FILING DATE: 5-JUN-1995
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                                                                                                          PFEHDEEIIKGQVFFRQTVSSECQHLIKWCLSLRPSDRPSFEEIRNHPWMQGDLLPQAAS
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EIHLHSLSPGPSK 313
                         EIHLHSLSPGSSK 313
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                                                                                   PFEHDEETIRGOVFFRORVSSECOHLIRWCLALRPSDRPTFEETONHPWMQDVLLPQETA
                                                                                                                                                                          ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI
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ID NO: 26:
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Pred. No. 8.6e-153;
0; Mismatches 9;
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Gaps

60

Folded Structures of Proteins

300

240

300

Switzerland

code)

CH-8092

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; JOURNAL: Scien
; VOLUME: 241
; PAGES: 42-52
; DATE: 1988
US-07-857-2248-41
RESULT 14
US-09-237-543-5
; Sequence 5, Application US/09237543A
; Patent No. 6143540
; GENERAL INFORMATION:
; APPLICANT: Kapeller, Rosana
; TITLE OF INVENTION: NOVEL MOLECULES OF THE HKID-1-RELATED |
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: 035800/175631
; CURRENT APPLICATION NUMBER: US/09/237,543A
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Best Local Similarity
Matches 256; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE: Protein kinase; Table 8 Column PUBLICATION INFORMATION: AUTHORS: Hanks, S. K. AUTHORS: Quinn, A. M. AUTHORS: Hunter, T. AUTHORS: Hunter, T. TITLE: The protein kinase family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 436
PRIOR APPLICATION DATA: none
TELECOMMUNICATION INFORMATION:
TELEPHONE: (International)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: (note: this is an international post code: COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette, 1.4 Mb storage COMPUTER: Apple MacIntosh
OPERATING SYSTEM: MacIntosh 7.0
SOFTWARE: Microsoft Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/857,224B
FILING DATE: 03/25/92
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DESCRIPTION:
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LENGTH: 257
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98.8%;
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Pred. No. 5.2e.
0; Mismatches
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CURRENT FILING DATE: 1999-01-26
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 455
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-09-237-543-5
                                                                                                                                                                                                                                                                                     SOFTWARE: PATENTIN
SEQ ID NO 5
LENGTH: 455
TYPE: PRT
ORGANISM: Rattus no
US-09-644-450-5
                                                                                                                                                                                                                                                                                                                                                                          Sequence 5, Application US/09644450
PALENT NO. 638791
GENERAL INFORMATION:
APPLICANT: Kapeller, Rosana
ITILE OF INVENTION: NOVEL MOLECULES OF THE
ITITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: 035800/175631
CURRENT APPLICATION NUMBER: US/09/644,450
CURRENT FILING DATE: 2000-08-23
NUMBER OF SEQ ID NOS: 11
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Matches 213
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Best Local Similarity
Matches 213; Conserv
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 305
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                                                                                                                                                                                                                                              Similarity
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               GIRVADNLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKV--SSDFSGVIRLLDWFER 112
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                                                                         PDSFVLILERPEPVQDLFDFITERGALQEDLARGFFWQVLEAVRHCHNCGVLHRDIKDEN
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                                                       PDGFLLVLER PEPAQDLFDF I TERGALDEPLARRF FAQVLAAVRHCHNCGVVHRD I KDEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LLVDLRSGELKLIDFGSGAVLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSATVWSLGVLL
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2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

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4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*

5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*

6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*
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US-10-348-081-14
US-10-664-421-2
US-10-705-757-6
US-10-971-791-9
US-09-971-791-9
US-09-971-791-9
US-09-971-791-9
US-10-348-081-12
US-09-971-791-9
US-10-664-421-13
US-10-664-421-13
US-10-664-421-15
US-10-971-791-98-18
US-10-951-406-18
US-10-951-664-635-152
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APPLICANT: Laura A. Rudolph-Owen
APPLICANT: Kyle MacBeth
TITLE OF INVENTION: NOVEL MOLECULES OF THE HK.
FILE REFERENCE: 35800/238856
CURRENT APPLICATION NUMBER: US/09/971,791
CURRENT FILING DATE: 2001-10-04
PRIOR APPLICATION NUMBER: 09/644,450
PRIOR TILING DATE: 2000-08-23
PRIOR FILING DATE: 1090-08-23
PRIOR APPLICATION NUMBER: 09/237,543
PRIOR APPLICATION NUMBER: 09/237,543
PRIOR FILING DATE: 1999-01-26
NUMBER OF SEQ ID NOS: 11
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 7.
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; TYPE: PRT
; ORGANISM: Mus musculus
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; Sequence 7, Application US/09971791
; Patent No. US20020115120A1
; GENERAL INFORMATION:
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                                                                                                                                        EIKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI
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US-10-705-757-11
US-10-377-268-14
US-10-941-635-6
US-10-941-635-6
US-10-971-791-5
US-09-971-791-5
US-09-971-791-664-421-166
US-10-425-114-54275
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Minimum Maximum

Searched:

Sequence:

Run on:

Database

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Sequence 2, Application US/10664421

Publication No. US20040142864A1

GENERAL INFORMATION:

APPLICANT: BREMER, RYAN

APPLICANT: HEACHIM, PRABHA

APPLICANT: MANDIYAN, VALSAN

APPLICANT: MANDIYAN, VALSAN

APPLICANT: MILBURN, MICHAEL V.

APPLICANT: MILBURN, MICHAEL V.

FIILE OF INVENTION: CRYSTAL STRUCTURE OF PIM-1 KINASE

FILE REFERENCE: 039363/0703

CURRENT APPLICATION NUMBER: US/10/664,421

CURRENT FILING DATE: 2003-09-16

PRIOR APPLICATION NUMBER: 60/412,341

PRIOR APPLICATION NUMBER: 60/412,341

PRIOR APPLICATION NUMBER: 60/413,398

PRIOR FILING DATE: 2002-09-20

PRIOR FILING DATE: 2002-09-16

NUMBER OF SEQ ID NOS: 169

SOCTUMEDE: DATE: 2003-09-16
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US-10-348-081-14
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Best Local Similarity
Matches 313; Conserv
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SEQ ID NO 14
LENGTH: 313
TYPE: PRT
ORGANISM: Mus musculus
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Publication No.
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APPLICANT: TSCHANK, Georg
TITLE OF INVENTION: PIM-3 KINASE AS A TARGET FOR TYPE 2 DIABETES MELLITUS
FILE REFERENCE: DEAVZ002/0004 US NP
CURRENT APPLICATION NUMBER: US/10/348,081
CURRENT FILING DATE: 2003-01-21
NUMBER OF SEQ ID NOS: 14
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APPLICANT: MUELLER, Guenter
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No. US20040038246A1
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100.0%; Pred. No. 8.1e-142;
ative 0; Mismatches 0;
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; LENGTH: 313
; TYPE: PRT
; ORCANISM: Mus musculus
US-10-664-421-2
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Sequence 6, Application US/1070577
Publication No. US20040146942A1
GENERAL INFORMATION:
APPLICANT: GRUENENTHAL GMBH
TITLE OF INVENTION: SCREENING METHOD USING PII
FILE REFERENCE: 029310.52818US
CURRENT APPLICATION NUMBER: US/10/705,757
CURRENT FILING DATE: 2003-11-12
PRIOR APPLICATION NUMBER: PCT/EP02/05234
PRIOR FILING DATE: 2002-05-13
PRIOR APPLICATION NUMBER: DE 101 23 055.9
PRIOR PILING DATE: 2001-05-11
                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 11
SEQ ID NO 6
SEQ ID NO 6
LENGTH: 313
TYPE: PRT
ORGANISM: Mus musculus
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Best Local Similarity 100.0%;
Matches 313; Conservative C
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Pred. No. 8.1e-142;
0; Mismatches 0;
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RESULT 6
US-10-941-635-2
; Sequence 2, Application US/10941635
; Publication No. US20050164300A1
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US-10-377-268-10
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PRIOR FILING DATE: 2003-01-02
PRIOR PELICATION NUMBER: 60/360,651
PRIOR FILING DATE: 2002-02-28
PRIOR APPLICATION NUMBER: 60/411,398
PRIOR APPLICATION NUMBER: 60/411,398
PRIOR FILING DATE: 2002-09-16
PRIOR APPLICATION NUMBER: 60/412,341
PRIOR APPLICATION NUMBER: 60/412,341
PRIOR FILING DATE: 2002-09-20
NUMBER OF SEQ ID NOS: 38
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO 10
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APPLICANT: MILBURN, MICHAEL VANCE
TITLE OF INVENTION: METHOD FOR THE DESIGN OF MOLECULAR SCAFFOLDS AND LIGANDS
FILE REFERENCE: 039363/0303
CURRENT APPLICATION NUMBER: US/10/377,268
CURRENT FILING DATE: 2003-02-28
CURRENT FILING DATE: 2003-02-28
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                                                                                          313
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Pred. No. 8.1e-142;
Mismatches 0;
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; LENGTH: 313
; TYPE: PRT
; ORGANISM: Mus m
US-10-941-635-2
; ORGANISM: Rattus US-09-971-791-8
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US-09-971-791-8
                                                                        GENERAL INFORMATION:

APPLICANT: Laura A. Rudolph-Owen

APPLICANT: Kyle MacBeth

TITLE OF INVENTION: NOVEL MOLECULES OF THE HKID-1-RELATED PROTEIN FAMILY AND USES

FILE REFERENCE: 3500/238856

CURRENT APPLICATION NUMBER: US/09/971,791

CURRENT FILING DATE: 2001-10-04

PRIOR APPLICATION NUMBER: 09/644,450

PRIOR APPLICATION NUMBER: 09/644,450

PRIOR APPLICATION NUMBER: 09/237,543

PRIOR APPLICATION NUMBER: 09/237,543

PRIOR FILING DATE: 1999-01-26

NUMBER OF SEQ ID NOS: 11

SOFTWARE: FastSEQ for Windows Version 4.0
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APPLICANT: ARTIS, DE
APPLICANT: BREMER,
APPLICANT: GILLETTE
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PRIOR FILING DATE: 2003-09-15
NUMBER OF SEQ ID NOS: 167
SOFTWARE: Patentin Ver. 3.2
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 8, Application US/09971791 Patent No. US20020115120A1
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Best Local :
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APPLICANT: IBRAHIM, PRABHA L.
APPLICANT: ZUCKERMAN, REBECCA L.
TITLE OF INVENTION: MOLECULAR SCAFFOLDS FOR KINASE LIGAND DEVELOPMENT
FILE REFERENCE: 039363-1702
CURRENT APPLICATION NUMBER: US/10/941,635
CURRENT FILING DATE: 2004-09-15
                                       LENGTH: 313
TYPE: PRT
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GILLETTE, SAMUEL J.
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US-10-348-081-12
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APPLICANT: WUELLER, Guenter
APPLICANT: SCHNEIDER, Rudolf
APPLICANT: SCHANK, Georg
TITLE OF INVENTION: PIM-3 KINASE AS A TARGET FOR TYPE 2 DIABETES MELLITUS
FILE REFERENCE: DEAV2002/0004 US NP
CURRENT APPLICATION NUMBER: US/10/348,081
CURRENT FILING DATE: 2003-01-21
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin version 3.2
SEQ ID NO 12
LENGTH: 313
TYPE: DET
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US-10-705-757-4
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CURRENT APPLICATION NUMBER: US/10/705,757
CURRENT FILING DATE: 2003-11-12
PRIOR APPLICATION NUMBER: PCT/EP02/05234
PRIOR FILING DATE: 2002-05-13
PRIOR FILING DATE: 2002-05-13
PRIOR APPLICATION NUMBER: DE 101 23 055.9
PRIOR FILING DATE: 2001-05-11
NUMBER: OF SEQ ID NOS: 11
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 4.313
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Publication No. US20040146942A1
GENERAL INFORMATION:
APPLICANT: GRUENENTHAL GMBH
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Patent No. US20020115120A1
GENERAL INFORMATION:
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Best Local Similarity
APPLICANT: Rosanna Kapeller-Libermann
APPLICANT: Laura A. Rudolph-Owen
APPLICANT: Kyle MacBeth
TITLE OF INVENTION: NOVEL MOLECULES OF THE HKID-1-RELATED PROTEIN FAMILY AND USES
FILE REFERENCE: 35800/238856
CURRENT APPLICATION NUMBER: US/09/971,791
CURRENT FILING DATE: 2001-10-04
PRIOR APPLICATION NUMBER: 09/644,450
PRIOR APPLICATION NUMBER: 09/643,450
PRIOR APPLICATION NUMBER: 09/237,543
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US-10-081-119-18
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                                                                                                      Query Match
Best Local Simi
Matches 294;
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Best Local S
Matches 294
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CURRENT FILING DATE: 2002-02-21
PRIOR APPLICATION NUMBER: 60/289,813
PRIOR FILING DATE: 2001-02-21
NUMBER OF SEQ ID NOS: 38
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 18
LENGTH: 313
                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Reinhard, Christoph
APPLICANT: Jefferson, Anne B.
APPLICANT: Jefferson Wivien W.
TITLE OF INVENTION: TTK in Diagnosis and as
TITLE OF INVENTION: Target in Cancer
FILE REFERENCE: 16932.002
                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 18, Application US/10081119 Publication No. US20030045491A1
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LENGTH: 31
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NUMBER OF SEQ ID NOS: 11
SOFTWARE: FastSEQ for Windows Version
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ORGANISM: Homo
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                                                                 MLLSKINSLAHLRARPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD
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93.9%; Pred. No. 4.6e-134;
tive 10; Mismatches 9;
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                                                                                                     Score 1582; DB 4;
Pred. No. 4.6e-134;
0; Mismatches 9;
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PRIOR FILING DATE: 2002-03-21
NUMBER OF SEQ ID NOS: 70
SOFTWARE: FASTSEQ for Windows Version 4
SEQ ID NO 52
                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 294; Conserv
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CURRENT APPLICATION NUMBER: US/10/394,322A
CURRENT FILING DATE: 2003-03-20
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APPLICANT: Prescott, John C.
TITLE OF INVENTION: IDENTIFICATION OF KINASE INHIBITORS
                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 313
TYPE: PRT
ORGANISM: Homo sapiens
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EIHLHSLSPGPSK 313
                           EIHLHSLSPGSSK 313
                                                                   PFEHDEEIIKGQVFFRQTVSSECQHLIKWCLSLRPSDRPSFEEIRNHPWMQGDLLPQAAS
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RESULT 13
US-10-348-081-13
; Sequence 13, Application US/10348081
; Publication No. US20040038246A1
; GENERAL INFORMATION:
; APPLICANT: KORN, Marcus

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APPLICANT: MUELLER, Guenter

APPLICANT: SCHNEIDER, Rudolf
APPLICANT: TSCHANK, Georg
TITLE OF INVENTION: PIM-3 KINASE AS A TARGET FOR TYPE 2 DIABETES MELLITUS
FILE REFERENCE: DEAV2002/0004 US NP
CURRENT APPLICATION NUMBER: US/10/348,081
CURRENT FILING DATE: 2003-01-21
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin version 3.2
SEQ ID NO 13
LENGTH: 313
TYPE: PRT
ORGANISM: Homo sapiens
US-10-348-081-13
                                                        APPLICANT: MANDIYAN, VALSAN
APPLICANT: MICHAEL V.
APPLICANT: MILBURN, MICHAEL V.
FILE OF INVENTION: CRYSTAL STRUCTURE OF PIM-1 KINASE
FILE REFERENCE: 039363/0703
CURRENT APPLICATION NUMBER: US/10/664,421
CURRENT FILING DATE: 2003-09-16
PRIOR APPLICATION NUMBER: 60/412,341
PRIOR FILING DATE: 2002-09-20
PRIOR APPLICATION NUMBER: 60/411,398
PRIOR PILING DATE: 2002-09-16
NUMBER OF SEQ ID NOS: 169
SOFTWARE: PALENTIN Ver. 3.2
SEQ ID NO 1
LENGTH: 313
TYPE: PRT
CRGANISM: Homo sapiens
US-10-664-421-1
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US-10-664-421-1
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Query Match
Best Local Sim
Matches 294;
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Best Local Similarity 93.9
Matches 294; Conservative
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APPLICANT: IBRAHIM, PRABH
APPLICANT: KUMAR, ABHINAV
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              94.8%;
; Score 1582; DB 4;
; Pred. No. 4.6e-134;
10; Mismatches 9;
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                              DB 4; Length 313;
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US-10-664-421-150
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Best Local Similarity 93.9%;
Matches 294; Conservative 1
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APPLICANT: MANDIYAN, VALSAN

APPLICANT: MILBURN, MICHAEL V.

FIILE OF INVENTION: CRYSTAL STRUCTURE OF PIM-1 KINASE

FILE REFERENCE: 039363/0703

CURRENT PILLO DATE: 2003-09-16

PRIOR APPLICATION NUMBER: 60/412,341

PRIOR APPLICATION NUMBER: 60/412,341

PRIOR FILLING DATE: 2002-09-20

PRIOR FILLING DATE: 2002-09-16

NUMBER OF SEQ ID NOS: 169

SOCTWARE: PATENTIN NUMBER: 60/411,398

PRIOR FILNG DATE: 2002-09-16

NUMBER OF SEQ ID NOS: 169

SOCTWARE: PATENTIN VET: 3.2

SEQ ID NO 150
                                                                                                            ; ORGANISM: Homo sapiens US-10-664-421-150
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APPLICANT: BREMER, RYAN
APPLICANT: IBRAHIM, PRABHA
APPLICANT: KUMAR, ABHINAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Application US/10664421
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; Score 1582; DB 4;
; Pred. No. 4.6e-134;
10; Mismatches 9;
                                                    Length 313;
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Indels

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Gaps

180

120 120 60

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Qy 301 EIHLHSLSPGSSK 313

Db 301 EIHLHSLSPGSSK 313

Search completed: May 4, 2006, 05:32:06

Job time: 93.6667 secs
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Result
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1: /SIDSS/ptodata/2/pubpaa/US06_NEW_PUB.pep1:*

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11 US-11-113-424-183

11 US-11-087-099-11500

12 US-11-087-099-11726

12 US-11-087-099-11726

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14 US-11-087-099-3612

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US-10-511-937-2982

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                                                Sequence 373, App Sequence 2982, Ap Sequence 32, Appl Sequence 40, Appl Sequence 90, Appl Sequence 690, Appl Sequence 77, Appl Sequence 72, Appl Sequence 11500, Ap Sequence 11726, A Sequence 11726, A Sequence 397, App Sequence 397, Ap Sequence 397, Ap Sequence 1183, A Sequence 12331, A Sequence 12331, A Sequence 12331, A
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Sequence 4237, Ap	Sequence 8358, Ap	Sequence 6, Appli	Sequence 877, App	Sequence 876, App	Sequence 880, App	Sequence 878, App	Sequence 881, App	Sequence 32576, A	Sequence 8865, Ap	Sequence 17, Appl	Sequence 65, Appl	Sequence 905, App	Sequence 20430, A	Sequence 20431, A	Sequence 3898, Ap	Sequence 10, Appl	Sequence 67, Appl	Sequence 18364, A	Sequence 1886, Ap	Sequence 12402, A	Sequence 7631, Ap	Sequence 32575, A	Sequence 951, App

## ALIGNMENTS

RESULT 1 US-10-784-004-373

Sequence 373, Application US/10784004

Publication No. US20060084066A1

GENERAL INFORMATION:

APPLICANT: Biogen Idec

TITLE OF INVENTION: Surrogate Markers of Pain
FILE REFERENCE: 08201.6029-00000

CURRENT APPLICATION NUMBER: US/10/784,004

CURRENT FILING DATE: 2004-02-20

NUMBER OF SEQ ID NOS: 1251

SOFTWARE: PatentIn version 3.2

SEQ ID NO 373

LENGTH: 455

TYEB: PRT

ORGANISM: rat
US-10-784-004-373 Ş Ś 밁 ঠ В Ş S 밁 밁 Query Match 67.3 Best Local Similarity 71.0 Matches 213; Conservative 305 173 365 233 245 113 186 130 MLLSKFGSLAHL----CGPGGVDHLPVKILQPAKADKESFEKVYQVGAVLGSGGFGTVYA S 1 MLLSKINSLAHLRARPC-----NDLHATKLAPGK-EKEPLESQYQVGPLLGSGGFGSVYS GIRVADNLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKV--SSDFSGVIRLLDWFER 112 PDSFVLILERPEPVQDLFDFITERGALQEDLARGFFWQVLEAVRHCHNCGVLHRDIKDEN GSRIADGLPVAVKHVVKERVTEWGSL-GGMAVPLEVVLLRKVGAAGGARGVIRLLDWFER YDMVCGDIPFEQDEEILRGRLFFRRRVSPECQQLIEWCLSLRPSERPSLDQIAAHPWMLG PDGFLLVLERPEPAQDLFDFITERGALDEPLARRFFAQVLAAVRHCHNCGVVHRDIKDEN 67.3%; Score 1122.5; DB 71.0%; Pred. No. 1.9e-90; 31; Mismatches DB 9; 43; Indels 13; Length = 455; Gaps 172 292 185 232 304 244 424 364 54

RESULT

US-10-511-937-2982

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FILE REFERENCE: 506612000104

CURRENT APPLICATION NUMBER: US/10/511,937

CURRENT FILING DATE: 2004-10-19

PRIOR APPLICATION NUMBER: PCT/US2003/012946

PRIOR APPLICATION NUMBER: PCT/US2003/012946

PRIOR APPLICATION NUMBER: US 10/131,831

PRIOR APPLICATION NUMBER: US 10/131,831

PRIOR APPLICATION NUMBER: US 10/325,899

PRIOR APPLICATION NUMBER: US 10/325,899

PRIOR APPLICATION NUMBER: US 10/325,899

PRIOR FILING DATE: 2002-12-20

NUMBER OF SEQ ID NOS: 3117

SOFTMARE: PatentIn version 3.2

SEQ ID NO 2982

LENGTH: 334

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US-10-511-937-2982
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Publication No. US2006008835A1
GENERAL INFORMATION:
APPLICANT: EXPRESSION DIAGNOSTICS, IN
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Best Local Similarity
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APPLICANT:
APPLICANT:
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APPLICANT: Rosenberg, Steven
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
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Ly, Ngoc
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APPLICANT: Mannion, Jane
APPLICANT: Clapper, Jonathan David
APPLICANT: Wang, Aijun
APPLICANT: Wang, Aijun
APPLICANT: Ordonez, Nadia
APPLICANT: Ordonez, Nadia
APPLICANT: Carter, Lauren
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Compositions and Methods for the Detection, Dia
TITLE OF INVENTION: Compositions and Methods for the Detection, Dia
TITLE OF INVENTION: And Therapy of Hematological Malignancies
FILE REFERENCE: 014058-014402PC
CURRENT APPLICATION NUMBER: US/10/501,841
CURRENT FILING DATE: 2003-07-14
PRIOR APPLICATION NUMBER: US 10/057,475
PRIOR APPLICATION NUMBER: WO PCT/US03/02353
PRIOR APPLICATION NUMBER: WO PCT/US03/02353
PRIOR FILING DATE: 2003-01-22
PRIOR APPLICATION SECONDATE: 2013-01-22
PRIOR APPL
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; ORGANISM: Homo sapiens
US-10-501-841-32
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APPLICANT: Gaiger, Alexander
APPLICANT: Algate, Paul A.
APPLICANT: Mannion, Jane
APPLICANT: Clapper, Jonathar
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SEQ ID NO 32
LENGTH: 334
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Query Match 51.0%;
Best Local Similarity 60.5%;
Matches 161; Conservative 38
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Best Local Similarity 59.6%;
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CURRENT FILING DATE: 2004-07-14
PRIOR APPLICATION NUMBER: US 10/057,475
PRIOR FILING DATE: 2002-01-22
PRIOR APPLICATION NUMBER: WO PCT/US03/02353
PRIOR FILING DATE: 2003-01-22
NUMBER OF SEO ID NOS: 124
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                      ORGANISM: Homo
                                                                                                                                                                                                                            TYPE: PRT
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; Score 850; DB 9; Length 311; ; Pred. No. 8.2e-67; 38; Mismatches 65; Indels
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RESULT 6
US-11-087-099-9816
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US-11-103-065-2
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SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 2
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/11/103,065
CURRENT FILING DATE: 2005-04-11
PRIOR APPLICATION NUMBER: US/10/184,563
PRIOR FILING DATE: 2002-06-27
PRIOR APPLICATION NUMBER: 60/301,702
PRIOR APPLICATION NUMBER: 60/301,702
PRIOR FILING DATE: 2001-06-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Meyers, Rachel E., Lora, Jose M.
TITLE OF INVENTION: 2150, Human Protein Kinase Family
TITLE OF INVENTION: Member and Uses Therefor
FILE REFERENCE: MPI2001-137PIRNM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
mes 161; Conserv
                                                                                                          266 LIKWCLSLRPSDRPSFEEIRNHPWMQ 291
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                                                                                                                                                                                                                                                                                                  LEVALLWKVGAGGGHPGVIRLLDWFETQEGFMLVLERPLPAQDLFDYITEKGPLGEGPSR 141
                                                                                                                                                                                                                                                                                                                    MEVVLLKKVSS--DFSGVIRLLDWFERPDSFVLILERPEPVQDLFDFITERGALQEDLAR 145
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LIKWCLSLRPSDRPSFEEIRNHPWMQ 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VYSPPEMIRYHRYHGRSAAVWSLGILLYDMVCGDIPFEHDEEIIKGQVFFRQTVSSECQH 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GFFWQVLEAVRHCHNCGVLHRDIKDENILIDLSRGEIKLIDFGSGALLKDTVYTDFDGTR 205
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                                                                                        LIRRCLAPKPSSRPSLEETLLDPWMQ 287
                                                                                                                                                          VYSPPEWISRHQYHALPATVWSLGILLYDMVCGDIPFERDQEILEAELHFPAHVSPDCCA 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VYSPPEWISRHQYHALPATVWSLGILLYDMVCGDIPFERDQEILEAELHFPAHVSPDCCA 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LEVALLWKVGAGGGHPGVIRLLDWFETQEGFMLVLERPLPAQDLFDYITEKGPLGEGPSR
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 Application US/11087099
                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                            51.0%; Score 850; DB 11; 60.5%; Pred. No. 8.2e-67; tive 38; Mismatches 65;
                                                                                                                                                                                                                                                                                                                                                                                                                                             65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 311;
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GENERAL INFORMATION:

APPLICANT: Ludwig Institute for Cancer Research et

TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES

FILE REFERENCE: 28967/39178

CURRENT APPLICATION NUMBER: US/10/505,928

CURRENT FILING DATE: 2004-08-27

PRIOR APPLICATION NUMBER: US 60/363,019

PRIOR APPLICATION NUMBER: US 60/363,019

PRIOR FILING DATE: 2002-03-07

NUMBER OF SEQ ID NOS: 866

SOFTWARE: PATENTIAL 3.2

SEQ ID NO 690
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US-10-505-928-690
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US-11-087-099-9816
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Abad, Mark S. et al.
TITLE OF INVENTION: Genes and Uses for Plant Improvement
FILE REFERENCE: 38-21(53450)B EP
CURRENT APPLICATION NUMBER: US/11/087,099
CURRENT FILING DATE: 2005-03-22
NUMBER OF SEQ ID NOS: 12464
SEQ ID NO 9816
LENGTH: 504
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 690, A Publication No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Publication No. US20060041961A1 GENERAL INFORMATION:
                                                                                                                                                                                                                              Best Local Similarity
                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                      ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                        LENGTH: 661
TYPE: PRT
105
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 217 RYHGRSAAVWSLGILLYDMVCGDIFFEHDEEI-----IKGQVF-FRQTVSSECQHLIKW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      122 CHRNMVVHRDLKPENLILD-SKCNVKIADFGLSNIMRDGHFLKTSCGSPNYAAPEVISGK 180
                                                                                                                                      48
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                                                                                                                                                                      31 KEPLESQYQVGPLLGSGGFGSVYSGIRVADNLPVAIKHVEKDRISDWGELPNGTRVPMEV 90
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             h 22.7%; Score 379; DB 11; Similarity 35.5%; Pred. No. 2.5e-25; 94; Conservative 47; Mismatches 108;
                                                          EIMS--SLNHPHIISIYEVFENKDKIVIIMEYASK-GELYDYISERRRLSERETRHFFRQ
                                                                                VLLKKVSSDFSGVIRLLDWFERPDSFVLILERPEPVQDLFDFITERGALQEDLARGFFWQ 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MLVVDPMKRITIPEIRQHPWFQAHL
                                                                                                                                    KHNLKHRYELQETLGKGTYGKVKRATERFSGRVVAIKSIRKDKIKDEQDM----VHIRREI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SDFSGVIRLLDWFERPDSFVLILERPEPVQDLFDFITERGALQEDLARGFFWQVLEAVRH
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                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                              22.7%; Score 378.5; DB 8; 34.6%; Pred. No. 3.9e-25;
                                                                                                                                                                                                             47; Mismatches 114;
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                                                                                                                                  104
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                                                                                                                        ; OTHER INFORMATION: Description of Artificial Sequence; OTHER INFORMATION: domain Consensus Sequence US-10-877-346-74
                                                                                                                                                                                                                                               SOFTWARE: PatentIn
SEQ ID NO 74
LENGTH: 256
                                          Query Match
Best Local Similarity
Matches 97; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILE REFERENCE: 21402-124
CURRENT APPLICATION NUMBER: US/10/877,346
CURRENT FILING DATE: 2004-06-25
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APPLICANT: MacDougall, John F
                                                                                                                                                                                                                                                                                                        Remaining Prior Application data removed - See File Wrapper or PALM NUMBER OF SEQ ID NOS: 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Shimkets, Richard A
TITLE OF INVENTION: Novel Proteins and Nucleic Acids Encoding Same
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
                                                                                                                                                                                            TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                        FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 60/235,808 FILING DATE: 2000-09-27 APPLICATION NUMBER: 60/236,064 FILING DATE: 2000-09-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 60/235,631 FILING DATE: 2000-09-27
                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 2000-10-03
APPLICATION NUMBER: 60/238,321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: 60/236,065
FILING DATE: 2000-09-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: 60/235,633 FILING DATE: 2000-09-27
                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 60/237,434
                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 2000-09-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 60/236,135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 2000-09-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 60/236,066
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     281 GLIRWMLMVNPDRRATIEDIANHWWV 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            265 HLIKWCLSLRPSDRPSFEEIRNHPWM 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  162 IVSAVHYCHKNGVVHRDLKLENILLD-DNCNIKIADFGLSNLYQKDKFLQTFCGSPLYAS
    38 YQVGPLLGSGGFGSVYSGIRVADNLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVS 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ellerman, Karen
Grosse, William M
Alsobrook II, John P
Lepley, Denise M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PEIVNGRPYRGPEVDSWALGVLLYTLVYGTMPFDGFDHKNLIRQISSGEYREPTQPSDAR 280
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Millet, 18an
Stone, David
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Padigaru, Muralidhara
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Smithson, Glennda
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                                            Conservative
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                                          22.4%; Score 373.5; DB 9; 36.6%; Pred. No. 3.2e-25; tive 45; Mismatches 100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   John R
                                            Indels
                                                                              Length
                                                                                                                                                                   Protein
                                            23;
                                          Gaps
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                                                                                                                                                                                                                                   CURRENT FILING DATE: 2004-06-25

PRIOR APPLICATION NUMBER: US/10/877,346

CURRENT FILING DATE: 2001-09-26

PRIOR APPLICATION NUMBER: 05/235,631

PRIOR APPLICATION NUMBER: 60/235,631

PRIOR FILING DATE: 2000-09-27

PRIOR PELICATION NUMBER: 60/235,633

PRIOR FILING DATE: 2000-09-27

PRIOR APPLICATION NUMBER: 60/235,808

PRIOR FILING DATE: 2000-09-27

PRIOR APPLICATION NUMBER: 60/236,064

PRIOR FILING DATE: 2000-09-27

PRIOR APPLICATION NUMBER: 60/236,064

PRIOR APPLICATION NUMBER: 60/236,065

PRIOR APPLICATION NUMBER: 60/236,066

PRIOR APPLICATION NUMBER: 60/236,066

PRIOR FILING DATE: 2000-09-27

PRIOR APPLICATION NUMBER: 60/236,066

PRIOR APPLICATION NUMBER: 60/236,066

PRIOR APPLICATION NUMBER: 60/236,135

PRIOR APPLICATION NUMBER: 60/237,434

PRIOR APPLICATION NUMBER: 60/237,434

PRIOR APPLICATION NUMBER: 60/237,434
                                                                                                SOFTWARE: PatentIn Ver. SEQ ID NO 72
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 72, Application US/10877346 Publication No. US20060014153A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Gerlach, APPLICANT: MacDouga
                                                                                                                                             Remaining Prior Application data removed - See File Wrapper or PALM. NUMBER OF SEQ ID NOS: 127
                                                                                                                                                                                             PRIOR APPLICATION NUMBER: 60/238,321 PRIOR FILING DATE: 2000-10-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILE REFERENCE:
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TYPE: PRT ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF
                                                                      ENGTH: 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     172 EGRGYSSK-VDVWSLGVILYELLTGKLPFPGIDPLEELFRIKERPRLRLPLPPNCSEELK 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   214 RYHRYHGRSAAVWSLGILLYDMVCGDIPF---EHDEEI--IKGQVFFR----QTVSSECQ 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     113 YLHSRGIVHRDLKPENILLD-ENGTVKIADFGLARKLESSSYEKLTTFVGTPEYMAPEVL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 56 -- HPNIVRLLGVFEEDDHLYLVMEYMEG-GDLFDYLRRNGLLLSEKEAKKIALQILRGLE 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98 SDFSGVIRLLDWFERPDSFVLILERPEPVQDLFDFITERG-ALQEDLARGFFWQVLEAVR 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              T: Shimkets, Richard A
INVENTION: Novel Proteins and Nucleic Acids Encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YELGEKLGSGAPGKVYKGKHKDTGEIVAIKILKKRSLSE----KKKRFLREIQILRRLS
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Smithson, Glennda
Millet, Isabelle
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Grosse, William M
Alsobrook II, John P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Spytek, Kimberly A
Leach, Martin D
Shimkets, Richard A
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Padigaru, Muralidhara
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Stone, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kekuda,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lepley, Denise M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gunther, Erik
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21402-124
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; OTHER INFORMA;
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US-10-877-346-72
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US-11-113-424-183
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PRIOR FILING DATE: 2000-12-19
PRIOR PPLICATION NUMBER: 60/311,590
PRIOR APPLICATION NUMBER: 60/311,590
PRIOR FILING DATE: 2001-08-10
PRIOR PPLICATION NUMBER: 60/257,314
PRIOR PPLICATION NUMBER: 60/311,613
PRIOR PPLICATION NUMBER: 60/311,613
PRIOR PILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: 60/307,506
PRIOR APPLICATION NUMBER: 60/307,506
PRIOR PILING DATE: 2001-09-24
PRIOR APPLICATION NUMBER: 60/322,358
PRIOR APPLICATION NUMBER: 60/294,075
PRIOR APPLICATION NUMBER: 60/294,075
PRIOR APPLICATION NUMBER: 60/294,075
                                                               Query Match
Best Local S
Matches 92
                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 190
SOFTWARE: PatentIn Ver. 2.
SEQ ID NO 183
LENGTH: 256
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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PRIOR APPLICATION NUMBER: 60/288,153
PRIOR FILING DATE: 2001-05-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILE REFERENCE: 21402-225
CURRENT APPLICATION NUMBER: US/11/113,
CURRENT FILING DATE: 2005-04-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Gangolli et al.
TITLE OF INVENTION: Polypeptides and Nucleic
                                                                                                                                       FEATURE:
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                     ORGANISM: Artificial Sequence
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R INFORMATION: S
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                                                               Similarity
92; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CHNCGVLHRDIKDENILIDLSRGEIKLIDFGSGALLKD--TVYTDFDGTRVYSPPEWIRY 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SDFSGVIRLLDWFERPDSFVLILERPEPVQDLFDFITERGALQEDLARGFFWQVLEAVRH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CQHLIKWCLSLRPSDRPSFEEIRNHPW 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GKGYGKAVDIWSLGVILYELLTGKPPFPGDDQLL---ALFKKIGKPPPPFPPPEWKISPE
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5. US20050260713A1
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Serine/Threoniune protein kinase Co
Sequence
                                                                                                                                                       Description
                                                                                                                                       sequence
                                                            22.3%;
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Pred. No. 4.8e-25;
                                                                                                                                                     of Artificial Sequence:
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                                                                                         DB 11;
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                                                              Gaps
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Sequence 357, Application 09/2005
Sequence 357, Application 09/2005
Publication No. US20060046249A1

Publication No. US20060046249A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT:
FIFTLE OF INVENTION:
ACTIVITY OF COMPOUNDS THAT INTERACT WITH PROTEIN TYROSINE KINAS
TITLE OF INVENTION:
ACTIVITY OF COMPOUNDS THAT INTERACT WITH PROTEIN TYROSINE KINAS
TITLE OF INVENTION:
AUD/OR PROTEIN TYROSINE KINASE PATHWAYS

TITLE OF INVENTION:
TITLE OF INVENTION:
AUD/OR PROTEIN TYROSINE KINASE PATHWAYS
                                                                                                                                                                  RESULT 12
US-10-501-035-357
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SEQ ID NO 11500
LENGTH: 514
TYPE: PRT
ORGANISM: Lycopersicon esculentum
US-11-087-099-11500
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US-11-087-099-11500
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Best Local (
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                                                                                                                                                                                                                                                             270
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22.2%;
                                                                                                                                                                                                                                275
                                                                                                                                                                                                                                                           294
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APPLICANT: Abad, Mark S. et al.
TITLE OF INVENTION: Genes and Uses for Plant
FILE REFERENCE: 38-21 (53450) B EP
CURRENT APPLICATION NUMBER: US/11/087,099
CURRENT FILING DATE: 2005-03-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LYAGPEVDVMSCGVILYALLCGTLPFD-DENIPNLFKKIKGGIYTLPSHLSAGARDLIPR
                                                                                 CHRNMVVHRDLKPENLLLD-SKWNVKIADFGLSNIMRDGHFLKTSCGSPNYAAPEVISGK 191
                                                                                                            CHNCGVLHRDIKDENILIDLSRGEIKLIDFGSGALLKDTVYTDFD-GTRVYSPPEWIRYH
                                                                                                                                                                                                  RYHGRSAAVWSLGILLYDMVCGDIPFEHDEEI----IKGQVF-FRQTVSSECQHLIKW
                                                                                                                                                                     HPH--IIRLYEVIETPSDIYVVMEYVKS-GELFDYIVEKGRLQEDEARNFFQQIISGVEY
                                                                                                                                                                                                                                                             YKLGKTLGIGSFGKVKIAEHTLTGHKVAVKILNRRKIRN----MDMEEKVRREIKILRLFM
                                                                                                                                                                                                                                                                                                        YOVGPLLGSGGFGSVYSGIRVADNLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LHSQGIIHRDLKPENILLD-SDGHVKLADFGLAKQLDSGGTLLTTFVGTPEYMAPE-VLL 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CHNCGVLHRDIKDENILIDLSRGEIKLIDFGSGALLKD--TVYTDFDGTRVYSPPEWIRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SDFSGVIRLLDWFERPDSFVLILERPEPVQDLFDFITERGALQEDLARGFFWQVLEAVRH
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                                                                                                                                                                                                                                                                                                                                               ; Score 370; DB 11;
; Pred. No. 1.6e-24;
50; Mismatches 108;
                                                                                                                                                                                                                                                                                                                                                                                          Length 514;
                                                                                                                                                                                                                                                                                                                                                    Indels
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Sequence 11726, Application US/11087099

Publication No. US20060041961A1

GENERAL INFORMATION:

APPLICANT: Abad, Mark S. et al.

TITLE OF INVENTION: Genes and Uses for Plant Improvement

FILE REFERENCE: 38-21(53450) B EP

CURRENT APPLICATION NUMBER: US/11/087,099

CURRENT FILING DATE: 2005-03-22

NUMBER OF SEQ ID NOS: 12464

SEQ ID NO 11726

LENGTH: 513

TYPE: PRT

ORGANISM: Hordeum vulgare
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/10/501,035
CURRENT FILING DATE: 2004-07-09
PRIOR APPLICATION NUMBER: US 60/350,061
PRIOR FILING DATE: 2002-01-18
NUMBER OF SEQ ID NOS: 795
SOFTWARE: PATENTIN VERSION 3.2
SEQ ID NO 357
LENGTH: 950
TYPE: PRT
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                               RVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDIPFEHDE-----EIIKGQVFFRQT-
                                                                                             GFFWQVLEAVRHCHNCGVLHRDIKDENILIDLSRGEIKLIDFGSGALLKDTVYTDFD-GT
                                                                                                                              --EIKIMRLFIDFIHPHIIRVYEVIETPKDIFVVMEYCNN-GELLDYIIENGRLQEDEAR
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Sequence 3997, Application US/11087099
PUBLICATION NO. US20060041961A1
GENERAL INFORMATION:
APPLICANT: Abad, Mark S. et al.
TITLE OF INVENTION: Genes and Uses for Plant Imperior REFERENCE: 38-21 (53450) B EP
CURRENT APPLICATION NUMBER: US/11/087,099
CURRENT FILING DATE: 2005-03-22
NUMBER OF SEQ ID NOS: 12464
SEQ ID NO 3997
LENGTH: 512
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US-11-087-099-3997
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US-11-241-056-11
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Matches 98
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn version 3.1 SEQ ID NO 11
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CURRENT FILING DATE: 2005-09-30
PRIOR APPLICATION NUMBER: US/09/980,464
PRIOR FILING DATE: 2001-11-27
NUMBER OF SEQ ID NOS: 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Immunex Corporation
APPLICANT: Bird, Timothy A.
APPLICANT: Virca, G. Duke
APPLICANT: Martin, Unja
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TYPE: PRT
ORGANISM: Mus
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TITLE OF INVENTION: NOVEL MURINE AND HUMAN KINASES
FILE REFERENCE: 2923-US
TYPE: PRT
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Gaps

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re greater than or equal to the score of the result being printed,
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ABR62936	AA019791	AAO20524	AEB96048	ADR88375	ADO60032	ABR62933	AAO19792	ADR88376	ADT07367	ADK71853	ADI57241	AAY43942	ADY85580	ADN03170	ADI57202	AAY87959	AAW08139	AEB96037	AEA89424	AUX86/82
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## ALIGNMENTS

RESULT 1

ABG33015
IID ABG3
XX ABG3
AC A differentiative disorder; cancer; Acute promyeloid leukaemia; APML; Waldenstrom's macroglobulinaemia; 26-JAN-1999; 23-AUG-2000; 04-OCT-2001; 2001US-00971791. 22-AUG-2002. Mus musculus HKID-1; serine/threonine kinase; cellular proliferative disorder; differentiative disorder; cancer; hasematopoietic neoplastic disor Acute promyceloid leukaemia; APML; Chronic myelogenous leukaemia; WM; mouse. ABG33015 standard; protein; 313 US2002115120-A1 Mouse protein 20-DEC-2002 ABG33015; (MILL-) MILLENNIUM PHARM INC. 2000US-00644450 (first entry) kinase phosphorylation site 9908-00237543 ₽

Modulating levels or activity of HKID-1 polypeptides, a member of serine/threonine kinase superfamily, for treating cancer, by contacting cell expressing the polypeptide with a modulator of the polypeptide.

WPI; 2002-712471/77.

Kapeller-Libermann R,

Rudolph-Owen LA,

Macbeth

×

Example 3; Page 38-39; 48pp; English.

The invention describes a method of modulating the level or activity of human HKID-1 polypeptide, a member of serine/threonine kinase superfamily. The method involves contacting a cell expressing the polypeptide or nucleic acid with an agent to modulate the level or activity of polypeptide, or level of nucleic acid molecule. The method is useful for modulating the level or activity of HKID-1 polypeptide or polynucleotide in a subject having or predisposed to having a disorder involving cancer. Modulating HKID-1 expression or activity is useful for therapeutic purposes, for treating cellular proliferative and/or

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Matches 313
The present invention relates to a method of identifying pain-regulating compounds, involving screening candidate compounds for interaction with
                                   Claim 11;
                                                      Method for identifying analgesics, useful particularly for treating chronic pain, by screening compounds for interaction with PIM-1 or kinase, or related compounds.
                                                                                                       N-PSDB;
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The present sequence is the protein sequence of the murine serine/threonine protein kinase and proto-oncogene, PIM-1. Fare the paralogues of novel human and murine PIM-3 proteins
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                                                                    New human or murine PIM-3 DNAs or polypeptides, useful for agent for identifying anti-type 2 diabetes mellitus drugs, treating insulin resistance or type 2 diabetes mellitus.
                                               Example 2;
                                                                                                                      WPI; 2003-598536/56
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ilarity 100.0%;
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Pred. No. 3.8
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3.8e-158;
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New transgenic mouse, useful as model system for the
                                                                                                                                                                                                                                           mouse; probasin;
Pim1.
                                                                                                                                                                                                                                                                                  Murine Pim1
                                                                                                                                                                                                                                                                                                                                                              ADN97347 standard; protein;
                           WPI; 2004-099050/10.
                                                                                                                                23-JUN-2003; 2003WO-US019818
                                                                                                                                                                                                                 Mus musculus
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                                                                                                         21-JUN-2002; 2002US-0390692P
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                                                                                CALIFORNIA.
                                                    Ellwood-Yen
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                                                                                                                                                                                                                                                     promoter; transgenic mouse; c-myc; prostate cancer;
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Pred. No. 3.8e-158;
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RESULT 5
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AC ADR8
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Mus
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Mole
KW G-pr
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OS Mus
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PN US20
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PD 02-S
XX
PF 28-F

scaffold; nuclear hormone receptor; TNF receptor; coupled receptor; methyl transferase; ligase; PIN

ligase;

PIM;

mouse

PIM 1 protein (first

entry)

28-FEB-2003; 2003US-00377268

02-SEP-2004.

Mus musculus G-protein coupled Molecular Mus musculus 18-NOV-2004 ADR88371 standard; protein;

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EIHLHSLSPGSSK 313

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   a nucleic acid construct comprising a promoter having a fully defined nucleotide sequence comprising 310 bp (ADN97341), where the promoter is operably linked to c-myc having a fully defined nucleotide sequence comprising 1320 bp (ADN97342) where the c-myc protein encoded is expressed in prostate cells of the transgenic mouse at detectable levels. The transgenic mouse can be used as an in vivo model system for the study of prostate cancer and its progression. It can also be used in preclinical and clinical models to test novel diagnostic and therapeutic modalities including drug therapies relevant to prostate cancer prevention and progression. The transgenic animal can also be used to identify molecular markers that can be mediators of progression. Indentification of the mediators is useful since they are potential
                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 313 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       therapeutic targets. The present sequence represents murine Pim1
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     EIHLHSLSPGSSK
                                  PFEHDEEIIKGQVFFRQTVSSECQHLIKWCLSLRPSDRPSFEEIRNHPWMQGDLLPQAAS
                                                       PFEHDEEIIKGQVFFRQTVSSECQHLIKWCLSLRPSDRPSFEEIRNHPWMQGDLLPQAAS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tits progression comprising a nucleic acid construct comprising operably linked to c-myc gene encoded in prostate cells of mouse.
                                                                                                                                                                                                                                                                                                                                                                       Conservative
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16-SEP-2002;
20-SEP-2002;
02-JAN-2003;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention relates to a method of designing a ligand binding to a target molecule. The method involves identifying as molecular scaffolds compounds binding to members of a molecular family, detecting orientation of scaffolds at a binding site of target, and synthesising ligand. The invention is useful for designing drug products and for designing ligand binding to target molecules such as nuclear hormone receptors, TNF receptors, G-protein coupled receptors, methyl transferases, ligases, etc. The present sequence is the Mus musculus PIN protein. This sequence is used to illustrate the method of invention.
Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Designing a ligand binding to a target molecule, comprises identifying molecular scaffolds compounds binding to members of a molecular family, detecting orientation of scaffolds at a binding site of target, and
                                   artery
                                                             Mouse
                                                                                     28-JUL-2005
                                                                                                                                    AEA19261 standard;
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                                    disease;
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; 2002US-0411398P.
; 2002US-0412341P.
; 2003US-0437929P.
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                                    vasotropic; arteriosclerosis; antiarteriosclerotic;
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Pred. No. 3.8e-158;
Mismatches 0;
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RESULT 7
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Best Local S
Matches 313
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Therapeutic agent for treating artery disease e.g., \epsilon comprises a component which inhibits the function of
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                                                micturition
                                                                                         20-OCT-2005
                                                                                                             AEB96041;
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                   Homo sapiens
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313; Conserv
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                                                                                                                                 standard;
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                                                                                                                                                                                               EIHLHSLSPGSSK
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                                       disorder;
in kinase;
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                                       urinary dysfunction; uropathic; gene serine-threonine kinase; enzyme.
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Pred. No. 3.8e-158;
Mismatches 0;
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DE102004004894-A1

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RESULT 8
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AC AEA1
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Best Local Similarity
Matches 313; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to a novel method for identifying substances that regulate urinary incontinence and the urge to urinate. The method comprises incubating a test compound with a cell and/or cell preparation that has synthesized a specific protein of the PIM (proviral integration site) kinase family and measuring either binding of the test compound to the PIM kinase, or a functional parameter that is altered by the binding. The method of the invention demonstrates uropathic and gene therapy incontinence and the urge to urinate. The method is based upon regulating the activity or expression of PIM kinases that are involved in bladder control. The current sequence is that of the house mouse PIM-1 serine-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Identifying substances that regulate PIM kinases, useful for treatment and diagnosis of urinary incontinence and the urge to urinate, and similar use of PIM proteins or nucleic acids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
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N-PSDB; AEB96040.
REFSEQ; NP_032868.
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              28-JUL-2005
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                                                            standard;
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              (first
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                                                            protein;
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              entry)
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Pred. No. 3.8e-158;
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bladder
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RESULT 9
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           Rat protein
                                    20-DEC-2002
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standard;

protein;

kinase phosphorylation

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entry)

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Query Match
Best Local 9
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                                                                                                                                                                                                                                                                                                           Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                       Therapeutic agent for comprises a component
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(KATA/)
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312; Conserv
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KATAKAMI N.
                                         PFEHDEEIIKGQVFFRQTVSSECQHLIKWCLSLRPSDRPSFEEIRNHPWMQGDLLPQAAS
                                                                                   313
             EIHLHSLSPGSSK
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EIHLHSLSPGSSK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KENKYUSHO
                                                                                                                                                                                                                                                                                                                                                                                                                      treating artery disease e.g., arteriosclerosis, which inhibits the function of protein Pim-1.
                    313
                                                                                                                                                                                                                                                                                                                                                                                               25pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              arteriosclerosis; antiarteriosclerotic;
                                                                                                                                                                                                                                                               Score 1662; DB 9;
Pred. No. 1.5e-157;
0; Mismatches 1;
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Best Local S
Matches 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention describes a method of modulating the level or activity of human HKID-1 polypeptide, a member of serine/threonine kinase superfamily. The method involves contacting a cell expressing the polypeptide or nucleic acid with an agent to modulate the level or activity of polypeptide, or level of nucleic acid molecule. The method is useful for modulating the level or activity of HKID-1 polypeptide or polynucleotide in a subject having or predisposed to having a disorder involving cancer. Modulating HKID-1 expression or activity is useful for therapeutic purposes, for treating cellular proliferative and/or differentiative disorders including cancer or necessarily cancer of the service of the servi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Modulating levels or activity of HKID-1 polypeptides, a member of serine/threonine kinase superfamily, for treating cancer, by contacting cell expressing the polypeptide with a modulator of the polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kapeller-Libermann R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26-JAN-1999; 99US-00237543.
23-AUG-2000; 2000US-00644450.
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EIHLHSLSPSPSK 313
                                        EIHLHSLSPGSSK 313
                                                                                     PFEHDEEIIKGQVFFRQTVSSECQHLIKWCLSLRPSDRPSFEEIRNHPWMQGDLLPQAAS
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Pred. No. 9.9e-150;
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Matches 295
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Method for identifying analgesics, useful particularly for treating chronic pain, by screening compounds for interaction with PIM-1 or kinase, or related compounds.
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N-PSDB; ABZ69187.
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                                                                                                   PFEHDEEIIKGQVFFRQTVSSECQHLIKWCLSLRPSDRPSFEEIRNHPWMQGDLLPQAAS
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        EIHLHSLSPGSSK 313
                                                              PFEHDEEIVKGQVYFRQRVSSECQHLIRWCLSLRPSDRPSFEEIQNHPWMQDVLLPQATA
                                                                                                                                                                            ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI
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Pred. No. 9.9e-150;
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                                                                                                                                                                                                                                                                                                                                 Sequence 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New human or murine PIM-3 DNAs or polypeptides, useful for as a screening agent for identifying anti-type 2 diabetes mellitus drugs, or for treating insulin resistance or type 2 diabetes mellitus.
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PFEHDEEIKGQVFFRQTVSSECQHLIKWCLSLRPSDRPSFEEIRNHPWMQGDLLFQAAS
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                                                                       EIKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI
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Pred. No. 9.9e.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     regulate urinary incontinence and the urge to urinate. The method comprises incubating a test compound with a cell and/or cell preparation that has synthesized a specific protein of the PIM (proviral integration site) kinase family and measuring either binding of the test compound to the PIM kinase, or a functional parameter that is altered by the binding. The method of the invention demonstrates uropathic and gene therapy applications and may be useful for treatment and diagnosis of urinary incontinence and the urge to urinate. The method is based upon regulating the activity or expression of PIM kinases that are involved in bladder control. The current sequence is that of the Norway rat PIM-1 serine-threonine kinase protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Identifying substances that regulate PIM kinases, useful for treatment and diagnosis of urinary incontinence and the urge to urinate, and similar use of PIM proteins or nucleic acids.
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N-PSDB; AEB96038.
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8; Mismatches 10;
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Matches 294
                                                                                                                                                                           related to tyrosine threonine kinase (TTK, see ABPS4938). TTK polynucleotides and polypeptides of the invention encompass polynucleotides and polypeptides having sequence similarity or sequence identity to human TTK and other genes and gene products related to TTK, such as Piml. The invention is based on the finding that TTK is differentially bressed in various forms of cancer. It provides methods for the identification of cancerous cells, especially breast cancer and colon cancer cells, by detection of expression levels of TTK, as well as diagnostic, prognostic and therapputic methods. These methods can be used as the basis of rational therapy. Assays for identifying molecules that modulate the activity of these genes in cancers, as well as methods of inhibiting tumour growth by inhibiting the activity of TTK are also
                                                                                                       Sequence
                                                                                                                                                           provided
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 80-81; 113pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         prostate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Reducing growth of cancer cells comprises reducing Tyrosine Threonine Kinase (TTK) activity, useful in diagnosing and treating disorders wi abnormal expression levels and activity of TTK, such as lung, colon,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Reinhard
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human Pimi.
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                 The invention describes a method of modulating the level or activity of human HKID-1 polypeptide, a member of serine/threonine kinase superfamily. The method involves contacting a cell expressing the polypeptide or nucleic acid with an agent to modulate the level or activity of polypeptide, or level of nucleic acid molecule. The method is useful for modulating the level or activity of HKID-1 polypeptide or polynucleotide in a subject having or predisposed to having a disorder involving cancer. Modulating HKID-1 expression or activity is useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HKID-1; serine/threonine kinase; cellular proliferative disorder; differentiative disorder; cancer; haematopoietic neoplastic disorder; Acute promyeloid leukaemia; APML; Chronic myelogenous leukaemia; CML; Waldenstrom's macroglobulinaemia; WM; human.
                                                                                                                                                                                                                               Modulating levels or activity of HKID-1 polypeptides, a member of serine/threonine kinase superfamily, for treating cancer, by contacting cell expressing the polypeptide with a modulator of the polypeptide.
                                                                                                                                                                                             Example 3;
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23-AUG-2000;
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2000US-00644450
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The present invention relates to a method of identifying pain-regulating compounds, involving screening candidate compounds for interaction with
                                                                                                                                    Method for identifying analgesics, useful particularly for treating chronic pain, by screening compounds for interaction with PIM-1 or kinase, or related compounds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAO19788 standard;
                                                                              Claim 1; Fig 1B; 97pp;
                                                                                                                                                                                                                                              WPI; 2003-120715/11.
N-PSDB; ABZ69186.
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## ALIGNMENTS

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C;Function: Catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threon A;Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threon C;Superfamily: kinase-related transforming protein; protein kinase homology C;Keywords: ATP; autophosphorylation; phosphotransferase; proto-oncogene; serine/threo: F;36-290/Domain: protein kinase homology <KIN> F;44-52/Region: protein kinase ATP-binding motif F;67/Active site: Lys #status predicted
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N;Alternate names: kinase-related transforming protein pim-1; pim-1 proto-oncogene pro
C;Species: Mus musculus (house mouse)
C;Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 09-Jul-2004
C;Accession: A24169
C;Accession: A24169
R;Selten, G.; Cuypers, H.T.; Boelens, W.; Robanus-Maandag, E.; Verbeek, J.; Domen, J.;
Cell 46, 603-611, 1986
A;Title: The primary structure of the putative oncogene pim-1 shows extensive homology
A;Reference number: A24169; MUID:86272109; PMID:3015420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Molecule type: DNA A;Residues: 1-313 <SEL> A;Residues: 1-313 <SEL> A;Cross-references: UNIPROT:P06803; UNIPARC:UPI00000294AF; GB:M13945; GB:M13946; NID:g C;Comment: Pim-1 autophosphorylates at unknown sites.
C;Genetics:
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A;Introns: 28/1; 63/3; 80/3; 203/1; 262/1
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EIHLHSLSPGSSK 313
                                                                                       PFEHDEEIIKGQVFFRQTVSSECQHLIKWCLSLRPSDRPSFEEIRNHPWWQGDLLPQAAS
                                                                                                                                                                EIKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI
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Pred. No. 3.7e-74;
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protein kinase (EC 2.7.1.37) pim-1 - human
N;Alternate names: kinase-related transforming protein pim-1; pi
C;Species: Homo sapiens (man)
C;Date: 31-Mar-1989 #sequence revision 07-Oct-1994 #text_change
C;Accession: JU0327; A46554; A27476; I58412
R;Reeves, R.; Spies, G.A.; Kiefer, M.; Barr, P.J.; Power, M.
Gene 90, 303-307, 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonin A; Note: in testis may be involved in signal transduction events of normal germ cell matu C; Superfamily: kinase-related transforming protein; protein kinase homology C; Keywords: ATP; autophosphorylation; phosphoprotein; phosphotransferase; proto-oncogene F; 36-290/Domain: protein kinase homology <KIN> F; 44-52/Region: protein kinase homology <KIN> F; 44-52/Region: protein kinase ATP-binding motif F; 46-7/Active site: Lys #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R;Wingett, D.; Reeves, R.; Magnuson, N.S. Nucleic Acids Res. 20, 3183-3189, 1992
A;Title: Characterization of the testes-specific pim-1 transcript A;Reference number: S26298; MUID:92319652; PMID:1620615
A;Accession: S26298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Species: Rattus norvegicus (Norway rat)
C;Date: 25-Feb-1994 #sequence_revision 21-Jan-1997 #text_change 09-Jul-2004
C;Accession: S26298
Gene 90, 303-307, 1990

A;Title: Primary structure of the putative human oncogene,
A;Reference number: JU0327; MUID:90382681; PMID:2205533
A;Accession: JU0327
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A; Residues: 1-313 <WIN>
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4.2e-70;
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Gene 54, 105-111, 1987

A;Title: The cDNA sequence and gene analysis of the human pim oncogene.

A;Title: The cDNA sequence and gene analysis of the human pim oncogene.

A;Reference number: A27476; MUID:87277423; PMID:3475233

A;Accession: A27476

A;Molecule type: mRNA

A;Residues: 1-14,'RA',17-313 <ZAK>

A;Cross-references: UNIPARC:UPI000014987C; GB:M16750; NID:g189956; PIDN:AAA60089.1; PID:

A;Cross-references: UNIPARC:UPI000014987C; GB:M16750; NID:g189956; PIDN:AAA60089.1; PID:

Concogene Res. 1, 103-112, 1987

A;Title: Comparison of the human and mouse PIM-1 cDNAs: Nucleotide sequence and immunolc

A;Title: Comparison of the human and mouse PIM-1 cDNAs: Nucleotide sequence and immunolc

A;Reference number: 158412; MUID:88217305; PMID:3329709

A;Accession: 158412

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Cross-references: UNIPARC:UPI0000001060; GB:M54915; NID:g189961; PIDN:AAA36447.1; PID:

C;Comment: Pim-1 autophosphorylates at unknown sites.
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AlMap position: 6p21.2-6p21.2

Allatrons: 28/2; 63/3; 80/3; 203/1; 262/1

C;Function: Catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonin C;Superfamily: kinase-related transforming protein; protein kinase homology C;Keywords: ATP; autophosphorylation; phosphoprotein; phosphotransferase; proto-oncogene F;36-290;Domain: protein kinase homology <KIN>
F;44-52/Region: protein kinase ATP-binding motif
F;67/Active site: Lys #status predicted
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A;Cross-references: UNIPROT:P11309; UNIPARC:UPI000001060; GB:M27903; NID:g189958; R;Meeker, T.C.; Nagarajan, L.; ar-Rushdi, A.; Croce, C.M.
J. Cell. Biochem. 35, 105-112, 1987
A;Title:Cloning and characterization of the human PIM-1 gene: a putative oncogene A;Reference number: A46554; MUID:88115604; PMID:3429489
A;Accession: A46554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Genetics:
A;Gene: GDB:PIM1
A;Cross-references: GDB:119495; OMIM:164960
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A; Residues: 1-313 <MEE>
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Best Local Similarity
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                                                                                                  ERPEPVQDLFDFITERGALQEDLARGFFWQVLEAVRHCHNCGVLHRDIKDENILIDLSRG
                                                                                                                                                                                                                                                                                                                                                                                                                                          NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSDFSGVIRLLDWFERPDSFVLIL
                                                                                                                                                                                                                               EIKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI
                                                                                                                                                                                                                                                                                                          ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG
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EIHLHSLSPGPSK
                                                  EIHLHSLSPGSSK 313
                                                                                                                                                                                                       ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI
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Pred. No. 5.2e-70;
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A;Reference number: 2
A;Accession: T22255
A;Status: preliminary
A;Molecule type: DNA
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R;van der Lugt, N.M.T.; Domen, J.; Verhoeven, E.; Linders, K.; EMBO J. 14, 2536-2544, 1995
A;Title: Proviral tagging in E-mu-myc transgenic mice lacking A;Reference number: S55333; MUID:95300786; PMID:7781606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Map position: X
A;Start codon: CTG
A;Note: locus between A-raf and Act-7, near Kv4.1
A;Pote: locus between A-raf and Act-7, near Kv4.1
C;Function:
A;Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threoning;Superfamily: kinase-related transforming protein; protein kinase homology
C;Superfamily: kinase-related transforming protein; phosphorylation; phosphoprotein; phosphotra
C;Keywords: alternative initiators; ATP; autophosphorylation; phosphoprotein; phosphotra
F;89-345/Domain: protein kinase homology <KIN>
F;97-105/Region: protein kinase ATP-binding motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Mccession: A43093
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 'M',27-370 <VA2>
A;Feridues: 'M',27-370 = VA12>
                                                          submitted to the EMBL Data A; Reference number: Z19538
                                                                                                                  hypothetical protein F45H7.4 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #t C;Accession: T22255
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A; Residues: 'M', 61-370
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A; Residues: 1-370 < VAN>
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Best Local :
Matches 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LRARPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVADNLPVAIKHVEK
                                                                                                                                                                                                                                                                                   EAELHFPAHVSPDCCALIRRCLAPKPCSRPSLEEILLDPWMQS---PAEEKPINSSKGSP
                                                                                                                                                                                                                                                                                                    KGQVFFRQTVSSECQHLIKWCLSLRPSDRPSFEEIRNHPWNQGDLLPQAASEIHLHSLSP
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                                                                                                                                                                                                                                                                                                                                                                                     GALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDIPFEHDEEII
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Pred. No. 3.4e-35;
1; Mismatches 87;
                    from
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                      GB/EMBL/DDBJ
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                                                                                                                                   #text_change
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A; Residues: 1-363 <WIL-
A; Cross-references: UNIDR
A; Experimental source: cl
C; Genetics:
A; Gene: CESP: F45H7.4
A; Introns: 72/3; 160/3; 3
A; Introns: 72/3; protein ki
                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein C06E8.3 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #t C;Accession: T15435 R;Favello, A.
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A;Cross-references: UNIPARC:UPI000017B744;
A;Cross-references: UNIPARC:UPI000017B744;
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A;Introns: 24/1; 7
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A; Residues: 1-409 < F.
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                                                                                                                                                                                                                                                                                                                                                 submitted to the EMBL Data Library, Februa A:Description: The sequence of C. elegans
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                                                                                                                                                                        Similarity
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               MLLSKINSLAHLRARPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD
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MERPANCMDLFDMVSVHGPLNEDMGKF1FKQVITTVFNMYSKHGLLHRDIKDENLIVNMN
                                                                             -NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSDFSGVIRLLDWFERPDSFVLI
                                                                                                       MIKRKLQDLAVCCSYQVDFLHEKK----HSVKEFKRKYEVLDEIGRGGFGIVYEATTRQD
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protein kinase
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76/3;
                                                                                                                                                           Conservative
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                                                                                                                                                                                                                                                                                                                                       Z18350
                                                                                                                                                                                                                                                                                                                                                                                                       #sequence_revision 20-Sep-1999 #text_change
                                                                                                                                                                                                              107/2; 145/3; 199/1;
                                                                                                                                                                       30.2%;
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Pred.
                                                                                                                                                                       Score 504; DB 2;
Pred. No. 6.5e-18;
                                                                                                                                                                                                                                                                                                                                                     February 1994
legans cosmid
                                                                                                                                                           Mismatches 124;
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                                                                                                                                                                                                                                                                                                              GB/EMBL/DDBJ
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No. 6.
                                                                                                                                                                                                                                                                   EMBL:U00034; NID:g458983;
                                                                                                                                                                                                               307/1; 375/1
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174
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179 175

RGEIKLIDFGSGALLKDTVYTDFDGTRVYSFPEWIRYHRYHGRSAAVWSLGILLYDMVCG

238

234

TGEVKLVDFGATAYAEKATKKEFQGTRSYCPPEWFRDQLYLPLEATSWSLGVLLFILLTG

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RESULT 8
A;Experimental source: cv.
C;Function:
A;Description: catalyzes th
C;Superfamily: SNF1-related
                                                                                                                         submitted to the EMBL Data Library, December A;Reference number: Z17020
A;Accession: T10449
                                                                                                                                                                                                       probable serine/threonine-specific protein kinase N,Alternate names: SNF1-related protein kinase C;Species: (Ocumis sativus (ocumber) C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C; Keywords: ATP F;71-324/Domain: F;79-87/Region:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mech. Dev. 48, 153-164, 1994

A;Title: Identification of novel protein kinases expressed A;Reference number: 149071; MUID:95200798; PMID:7893599 A;Accession: 149072
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein kinase - mouse (fragment)
c;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Oct-2004
C;Accession: I49072
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT
I49072
                                                                             A; Molecule type: mRNA
A; Residues: 1-504 < GUM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R; Ruiz, J.C.; Conlon, F.L.; Robertson, E.J.
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                                                                A; Cross-references: UNIPROT: P93113; UNIPARC: UPI00000A4B92; EMBL: Y10036
                                                                                                            A; Status: preliminary; translated
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Best Local S
Matches 104
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                                                                                                                                                                           N.J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                 VCGDI PFEHD----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LSRGEIKLIDFGSGALLK-DTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VLILERPEPVQDLFDFITERGALQEDLARGFFWQVLEAVRHCHNCGVLHRDIKDENILID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RVADNLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSDFSGVIRLLDWFERPDSF
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catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threoning SNF1-related protein kinase; protein kinase homology
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                                              Masterpiece;
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Pred. No. 2e-12;
                                                                                                              from
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les 91; Conserv
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   1069
                                                                1009
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                                                                                                                                                                                                                                                                                                                      Conservative
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A;Molecule type: DNA
A;Residues: 1-1101 <ANS>
A;Residues: 1-1101 <ANS>
A;Cross-references: UNIPROT:Q08217; UNIPARC:UPI00001
A;Cross-references: Strain S288C
C;Genetics:
A;Cross-references: SGD:S0005405
A;Cross-references: SGD:S0005405
C;Keywords: ATP
C;Keywords: ATP
F;839-1099/Domain: protein kinase ATP-binding motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R;Ansorge, W.; Benes, V.; Rechmann, S.; Schwager, C.; submitted to the Protein Sequence Database, July 1996 A;Reference number: S66723
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 9
$66730

R;Ansorge, W.; Benes, V.; Rechmann, S.; Schwager, C.; Teodoru, C.; Voss, H.

R;Ansorge, W.; Benes, V.; Rechmann, S.; Schwager, C.; Teodoru, C.; Voss, H.
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                                                                                                                                                                                                                                                                                                                                                                                                                     36 SQYQVGPLLGSGGFGSVYSGIRVADNLPVAIKHVEKDRI--SDW-----GELPNGTRVP
                                                                                                                                                                                                              DLARGFFWQVLEAVRHCHNCGVLHRDIKDENILIDLSRGEIKLIDFGSGALLKDTVYTDF
                                                                                            VGTMDYAAPEVLGGSSYKGKPQDIWALGVLLYTIIYKENPYYNIDEILEGELRFDKSEHV
                                                                                                                                                                                   HEAKLVFKQVVASIKHLHDQGIVHRDIKDENVIVD-SHGFVKLIDFGSAAYIKSGPFDVF
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SEECISLIKRILTREVDKRPTIDEIYEDKWLK 1100
                                           SSECOHLIKWCLSLRPSDRPSFEEIRNHPWMQ 291
                                                                                                                                                                                                                                                                               --MATLNKNSQE--NILKLLDFFEDDDYYYI----ETPVHGETGSIDLFDVIEFKKDMVE
                                                                                                                                                                                                                                                                                                                                                                         SDFTILQVMGEGAYGKVNLCIHNREHYIVVIKMIFKERILVDTWVRDRKLGTIPSEIQI-
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                                                                                                                                     DGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDIPFEHDEEIIKGQVFFRQT--V
                                                                                                                                                                                                                                                                                                                           MEVVILKKVSSDFSGVIRLLDWFERPDSFVLILERPEPVQ-----DLFDFITERGALQE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22.7%; Score 379; DB 2;
33.5%; Pred. No. 1.6e-11;
tive 60; Mismatches 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             47;
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Pred. No. 8.3e-12;
17; Mismatches 108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             UNIPARC: UPI000012DF35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     294
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C;Genetics: A;Gene: AKin10; AK21
A;Introns: 64/1; 125/3; 186/3; 230/3; 292/3; 322/3; 350/3; C;Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Nolecule type: DNA
A; Residues: 144-198 < TH2>
A; Cross-references: UNIPARC: UPI000009DEEO;
A; Cross-references: UNIPARC: UPI00009DEEO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Molecule type: DNA,
A;Residues: 144-198 «THU>
A;Residues: UNIPARC:UPI00009DEE0; EMBL:X86966; N
A;Cross-references: UNIPARC:UPI00009DEE0; EMBL:X86966; N
R;Thuemmler, F.; Kirchner, M.; Teuber, R.; Dittrich, P.
Plant Mol. Biol. 29, 551-565, 1995
A;Title: Differential accumulation of the transcripts of A;Reference number: S66314; MUID:96123233; PMID:8534852
A;Accession: S66334
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threoning C;Superfamily: SNF1-related protein kinase; protein kinase homology C;Keywords: ATP; magnesium; phosphotransferase; serine/threonine-specific protein kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: UNIPROT:Q38997; UNIPARC:UPI000012DE43; R;Thuemmler, F.; Kirchner, M.; Teuber, R.; Dittrich, P. submitted to the EMBL Data Library, May 1995
A;Description: Differential accumulation of the transcript
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Reference number: A; Accession: JC1446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R; LeGuen, L.; Thomas, M.; Bianchi, M.; Halford, N.G.; Kreis, Gene 120, 249-254, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change
C;Accession: JC1446; S58266; S66334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    serine/threonine-specific protein kinase (EC 2 N;Alternate names: protein kinase SNF1 homolog C;Species: Arabidopsis thaliana (mouse-ear cre
  밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Status: preliminary
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A; Residues: 1-512 < LEG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Title: Structure and expression of a gene from Arabidopsis A; Reference number: JC1446; MUID:93013041; PMID:1339373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local S
Matches 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;17-271/Domain: protein kinase homology <KIN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10
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  245
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                                                                                                                                                                                                                             LEAVRHCHNCGVLHRDIKDENILIDLSRGEIKLIDFGSGALLKDTVYTDFD-GTRVYSPP
                                                                                                                                                                                                                                                                                                                             LLKKVSSDFSGVIRLLDWFERPDSFVLILERPEPVQDLFDFITERGALQEDLARGFFWQV 151
                                                                                                                                                                                                                                                                                                                                                                            ESILPNYKLGRTLGIGSFGRVKIAEHALTGHKVAIKILNRRKIKN---MEMBEKVRREIK
                                                                                                                                                                                                                                                                                                                                                                                                                        EPLESQYQVGPLLGSGGFGSVYSGIRVADNLPVAIKHVEKDRISDWGELPNGTRVPMEVV
RDLIPRMLVVDPMKRVTIPEIRQHPWFQAHL
                                                                                                                                                                                                                                                                              ILRLFMHPH--IIRLYEVIETPTDIYLVMEYVNS-GELFDYIVEKGRLQEDEARNFFQQI
                                            QHLIKWCLSLRPSDRPSFEEIRNHPWMQGDL
                                                                                           EVISGKLYAGPEVDVWSCGVILYALLCGTLPFD-DENIPNLFKKIKGGIYTLPSHLSPGA
                                                                                                                                         EWIRYHRYHGRSAAVWSLGILLYDMVCGDIPFEHDEEI---
                                                                                                                                                                                   ISGVEYCHRNMVVHRDLKPENLLLD-SKCNVKIADFGLSNIMRDGHFLKTSCGSPNYAAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22.4%; Score 373; DE 34.7%; Pred. No. 1.6e tive 47; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          of the transcripts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL:X86966; NID:g928909; PIDN:CAA60529.1;
role in a signal transduction cascade regula
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL:X86966; NID:g928909; Dittrich, P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cress)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1;
L.6e-11;
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  275
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hypothetical protein 22E5.8 - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 09-Jul-2004
C;Accession: T13741
R;Murphy, L.; Harris, D.; Barrell, B.
submitted to the EMBL pata Library, April 1999
A;Reference number: Z17668
A;Reference number: Z17668
A;Accession: T13741
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A;Introns: 205/3; 227/1; 322/3; 688/3;
A;Note: EG:22E5.8
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A;Molecule type: DNA
A;Residues: 1-1398 <MUR>
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C;Genetics:
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           preliminary; translated from GB/EMBL/DDBJ
362
                                  260
                                                                     302
                                                                                                     206
                                                                                                                                        243
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                                                                                                   VYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDIPFEHD-----
SSECEHLIRRMLVLEPTRRYTIDQIKRHRWMCPELL
                                SSECONLIKWCLSLRPSDRPSFEEIRNHPWMQGDLL
                                                                     PYAAPEVFEGKOYTGPEIDIWSLGVVLYVLVCGALPFDGSTLOSLRDRVLSGRFRIPFFM
                                                                                                                                        KFWQIISAVEYCHKKGIVHRDLKAENLLLDLNM-NIKIADFGFSNHFKPGELLATWCGSP
                                                                                                                                                                       FFWQVLEAVRHCHNCGVLHRDIKDENILIDLSRGEIKLIDFG-SGALLKDTVYTDFDGTR
                                                                                                                                                                                                           YREVEIMKRLKHPH--IIKLYQVMETKNMIYIVSEYASQ-GEIFDYIAKYGRMSESAARF
                                                                                                                                                                                                                                            PWEVVLLKKVSSDFSGVIRLLDWFERPDSFVLILERPEPVQDLFDFITERGALQEDLARG
                                                                                                                                                                                                                                                                                KLKEPMRVGFYDIERTIGKGNFAVVKLARHRITKN-EVAIKIIDKSQL-----DQTNLQKV
                                                                                                                                                                                                                                                                                                                 KEKEPLE-SQYQVGPLLGSGGFGSV-YSGIRVADNLPVAIKHVEKDRISDWGELPNGTRV
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Pred.
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                                                                                                                                                                                                                                                                                                                                                                                                                                         782/3;
                                                                                                                                                                                                                                                                                                                                                                  373; DB 2;
No. 3.8e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                         814/2;
                                                                                                                                                                                                                                                                                                                                                   109;
397
                                                                                                                                                                                                                                                                                                                                                                                 Length 1398;
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                                                                                                     EEIIKGQVFFRQTV
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                                                                                                                                                                                                                                              146
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A;Residues: 1-1358 <CLA>
A;Cross-references: UNIPOT: P31374; UNIPARC: UPI000017A449; EMBL: L05146
R;Ouellette, F.; Clark, M.W.; Keng, T.; Storms, R.K.; Zhong, W.; Zeng,
submitted to the EMBL Data Library, January 1993
A;Description: Sequencing of Chromosome I from Saccharomyces cerevisiae
A;Reference number: S36711
A;Accession: S36717 probable serine/threonine protein kinase (EC 2.7.1.-) - yeast (Saccharomyces N;Alternate names: protein YAL002; protein YAL017w; secretory protein SSP138 C;Species: Saccharomyces cerevisiae C;Date: 30-Sep-1993 #sequence revision 02-Aug-1994 #text\_change 05-Oct-2004 C;Accession: S33653; S36717; S36732; JH0486 R;Clark, M.W.; Zhong, W.W.; Keng, T.; Storms, R.K.; Ouellette, B.F.F.; Barton Yeast 9; 543-549, 1993 Yeast 9; 543-549, 1993 A;Title: The YAL017 gene on the left arm of chromosome I of Saccharomyces cere, Reference number: S33653; MUID:93311122; PMID:8322517 RESULT S33653 A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-864,867-1358 <OUE>
A;Residues: 1-864,867-1358 <OUE>
A;Residues: 1-864,867-1358 <OUE>
A;Cross-references: UNIPARC:UPI000052EA6; EMBL:L05146; NID:g171851; PIDN:AAC04940.1;
A;Cross-references: UNIPARC:UPI0000052EA6; EMBL:L05146; NID:g171851; PIDN:AAC04940.1;
A;Cross-references: UNIPARC:UPI000052EA6; EMBL:L05146; NID:g171851; VID:g171851; VID:g R;Clark, M.W.; Zhong, V Yeast 8, 133-145, 1992 A;Title: Identification A;Reference number: S22 A; Accession: S33653 A; Molecule type: DNA A;Status: nucleic Identification of a Saccharomyces nce number: \$22266; MUID:92221690; number: 1: S36732 acid sequence not shown Cerevisiae homolog PMID:1561836 cerevisiae: B.F.F.; Barton, SNF2 transcription B.; cerevisiae Fortin, cerevisia of. z

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RESULT 11

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A;Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonir C;Superfamily: SNPl-related protein kinase; protein kinase homology C;Keywords: ATP; magnesium; phosphotransferase; serine/threonine-specific protein kinase F;17-271/Domain: protein kinase homology <KIN> F;25-33/Region: protein kinase ATP-binding motif F;48,67,142,144/Active site: Lys, Glu, Asp, Lys #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             serine/threonine-specific protein kinase (EC 2.7.1.-) NPK5 - C;Species: Nicotiana tabacum (common tobacco) C;Date: 28-Apr-1995 #sequence_revision 28-Apr-1995 #text_chan C;Accession: A5609 R;Muranaka, T.; Banno, H.; Machida, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;Sidhu, R.S.; Mathewes, S.; Bollon, A.P. Gene 107, 111-118, 1991
A;Title: Selection of secretory protein-encoding genes | A;Reference number: JH0483; MUID:92077420; PMID:1743509
A;Accession: JH0486
                                                                                                                                                                                                                                                                                                                                            A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-511 <MUR>
A;Cross-references: UNIPROT:Q40544; UNIPARC:UPI00000AADOC; GB:D26602; NID:g496384;
C;Function:
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A56009
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A;Residues: 1-72, 'E', 74-154 <SID>
A;Cross-references: UNIPARC:UPI000017A44B
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A;Molecule type: DNA
A;Residues: 1-862 <CL2>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              tase of Saccharomyces cerevisiae. A; Reference number: A56009; MUID:94217693; PMID:8164654
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A;Map position: 1L
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Matches 88
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54; Mismatches 100;
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C;Accession: T52633

R;Bhalerao, R.P.; Salchert, K.; Bako, L.; Okresz, L.; Szabados, L.; Muranana, Proc. Natl. Acad. Sci. U.S.A. 96, 5322-7, 1999

A;Title: Regulatory interaction of PRL1 WD protein with Arabidopsis SNF1-like A;Reference number: Z25116; MUID:99238528; PMID:10220464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Molecule type: mRNA
A;Residues: 1-512 <BHA>
A;Cross-references: UNIPROT:P92958; UNIPARC:UPI00000AC16D;
A;Experimental source: cultivar Columbia
C;Genetics:
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C; Function:
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C;Function: Catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonin A;Description: Catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonin C;Superfamily: SNF1-related protein kinase; protein kinase homology C;Keywords: ATP; magnesium; phosphotransferase; serine/threonine-specific protein kinase F;15-272/Domain: protein kinase homology <KIN>F;23-31/Region: protein kinase ATP-binding motif F;46,65,143,145/Active site: Lys, Glu, Asp, Lys #status predicted F;148,152/Binding site: magnesium (Asn, Asp) #status predicted
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submitted to the EMBL Data Library, April 1992
A;Reference number: S24578
A;Recession: S24579
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A;Title: Molecular analyses of a barley multigene family homologous to the yeast proteir A;Reference number: S60303; MUID:93258420; PMID:1302632
A;Accession: S60304
Search completed: May 4, 2006, 05:25:51 Job time: 21.3333 secs
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A;Residues: 1-61'A',63-513 <HA2>
A;Cross-references: UNIPARC:UPI00000A3F6F; EMBL:X65604; NID:gl8933; PIDN:CAA46554.1; PII
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A;Residues: 1-513 <HAL>
A;Cross-references: UNIPROT:Q40030; UNIPARC:UPI000017255D; EMBL:X65604
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C;Date: 19-Mar-1997 #sequence_revision 15-Aug-1997 #text_change 05-Oct-2004
C;Accession: S60304; S24579
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Local Similarity 34.1%;
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RC STRAIN-C27BL/6; TISSUE-Brain, and Eye;

RC MEDLINE-C2388257; pubMed=12477932; DOI=10.1073/pnas.242603899;

RS Strausberg R.L., Feingold E.A., Garcer L., Shenmen C.M., Schuler G.D.,

RIAUSER R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hong L.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hong L.,

A Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

A Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

A Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

A Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
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Best Local Sim
Matches 313;
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Q8CFN8;
01-MAR-2003 (
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ACT SITE
BINDING
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01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
10-MAY-2005 (TrEMBLrel. 30, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS00107; PROTEIN KINASE_ATP; 1.
PROSITE; PS50011; PROTEIN KINASE_DOM; 1.
PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
ATP-binding; Kinase; Nuclear protein; Nucleotide-binding; Phosphorylation; Proto-oncogene; Serine/threonine-protein Transferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Muridae; Murinae; Mus. NCBI_TaxID=10090;
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Mammalia, Eutheria,
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ATP (By similarity).
Proton acceptor (By similarity).
ATP (By similarity).
ATP (By similarity).
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Pred. No. 2
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ProDom; PD00001; Prot kinase; 1.

SMART; SM00220; S_TKC; 1.

R PROSITE; PS00107; PROTEIN KINASE ATP; 1.

R PROSITE; PS50011; PROTEIN KINASE ST; 1.

R PROSITE; PS00108; PROTEIN KINASE ST; 1.

R PROSITE; PS00108; PROTEIN KINASE ST; 1.

W ATP-binding; Kinase; Nucleotide-binding;

W Serine/threonine-protein kinase; Transferase.

W Serine/threonine-protein kinase; Transferase.
                                                                                                                                                                                                                                                                                              Query Match
Best Local S
Matches 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -:- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
-!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
EMBL; BC042885; AAH42885.1; -; mRNA.
EMBL; BC053016; AAH53019.1; -; mRNA.
EMBL; BC053016; AAH5316.1; -; mRNA.
SMR; O8CFN8; 32-308.
Ensembl; ENSMUSGnoool
                                                                                                                                                                                                                                                                                                                                                                                                                                                 MGI; MGI; 97584; Pini.
GG; GG:0005524; F:ATP binding; IEA.
GG; GG:0004674; F:Protein serine/threonine kinase activity;
GG; GG:0006468; P:protein amino acid phosphorylation; IEA.
InterPro; IPR000719; Prot_kinase.
InterPro; IPR008271; Ser_thr_pkin_AS.
InterPro; IPR008271; Ser_thr_pkinase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Strausberg R.;
Submitted (JUN-2003)
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Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=C57BL/6; TISSUE=Brain;
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                     EIHLHSLSPGSSK
                                             PFEHDEEIIKGQVFFRQTVSSECQHLIKWCLSLRPSDRPSFEEIRNHPWMQGDLLPQAAS
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                                                                                                                                                               ERPEPVQDLFDFITERGALQEDLARGFFWQVLEAVRHCHNCGVLHRDIKDENILIDLSRG
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l. Acad. Sci. U.S
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ProDom; PD000001; Prot kinase; 1.

PROSITE; PS00107; PROTEIN KINASE ATP; 1

PROSITE; PS50011; PROTEIN KINASE DOM; 1

PROSITE; PS00108; PROTEIN KINASE ST; 1.
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"The CDNA sequence of the feline pim-1 oncogene.";
Submitted (OCT-2001) to the EMBL/GenHank/DDBJ data
-!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a
-!- SUBCILIULAR LOCATION: Cytoplasmic and nuclear
-!- SUBCELLULAR LOCATION: Cytoplasmic and nuclear
-!- FTM: Autophosphorylated (By similarity).
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Q95LJ0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Felis silvestris catus (Cat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Felidae;
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SMR; Q95LJ0; 32-308.
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28-FEB-2003 (Rel. 41, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
Proto-oncogene serine/threonine-protein kinas
                                                                                                                                                                                                                                                                                                                                                                                                      Local - 295;
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PFEHDEEIIKGQVFFRQTVSSECQHLIKWCLSLRPSDRPSFEEIRNHPWMQGDLLPQAAS
                                                               ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI
                                                                                          EIKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI
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ATP (By similarity).
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ATP (By similarity).
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01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
Proto-oncogene serine/threonine-protein kinase
                                                                                                                                                                                                                                                                                                                                                                                          RGD; 3330; Pim1.
InterPro; IPR000719; Prot kinase.
InterPro; IPR000271; Ser Thr_pkin_AS.
Pfam; PF00069; Pkinase; I.
ProDom; PD000001; Prot kinase; 1.
PROSITE; PS00107; PROTEIN KINASE_DOM; 1.
PROSITE; PS00108; PROTEIN_KINASE_DOM; 1.
PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
ATP-binding; Kinase; Nuclear protein; Nucleotide-binding;
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PIR; S26298; S26298.
SMR; P26794; 32-308.
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"Characterization of the testes-specific pim-1 tra

Nucleic Acids Res. 20:3183-3189(1992).

-!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a

-!- SUBUNIT: Binds to RP9 (By similarity).

-!- SUBCILILLAR LOCATION: Cytoplasmic and nuclear

-!- PTW: Autophosphorylated (By similarity).

-!- SIMILARITY: Belongs to the Ser/Thr protein kin
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STRAIN=Sprague-Dawley; TISSUE=Tes
MEDLINE=92319652; PubMed=1620615;
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Rattus norvegicus (Rat).
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[3]
NUCLEOTIDE SEQUENCE.
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Zakut-Houri R., Hazum S., Gi
"The CDNA sequence and gene
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NUCLEOTIDE SEQUENCE.

MEDLINE=90382681; PubMed=2205533; DOI=10.1016/0378-1119(90)90195-W;

Reeves R., Spies G.A., Kiefer M., Barr P.J., Power M.;

"Drimary structure of the putative human oncogene, pim-1.";
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Eukaryota; Metazoa; (
Mammalia; Eutheria; E
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                                                                                                                                                                                                                                                                                                  Meeker T.C., Nagarajan L., Ar-Rushdi A., Cr
"Cloning and characterization of the human
oncogene related to the protein kinases.",
J. Cell. Biochem. 35:105-112(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=88217305; PubMed=3329709; Domen J., von Lindern M., Hermans
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EMBL; M27903; AAA60090.1; -; Genomic EMBL; M16750; AAA60089.1; -; mRNA. EMBL; M54915; AAA36447.1; -; mRNA. EMBL; M24779; AAA81553.1; -; mRNA. EMBL; BC020224; AAH20224.1; -; mRNA. EMBL; AF386792; AAK70871.1; -; Genom: PIR; JU0327; TVHUP1.

PDB; 1XQZ; X-ray; A=14-313.

PDB; 1XWS; X-ray; A=14-313.

PDB; 1XWS; X-ray; A=14-313.
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Ionov Y., Le X., Tunquist B.J., Sweetenham J.,
Johnson T., Lilly M.B., Kraft A.S.;
"Pim-1 protein kinase is nuclear in Burkitt's
localization is necessary for its biologic eff
Anticancer Res. 23:167-178 (2003)
-i- FUNCTION: Thought to play a role in signal
cells. May affect the structure or silenci
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MEDLINE=21154098; PubMed=11460166; DOI=10.1038/35085588;

Pasqualucci L., Neumeister P., Goossens T., Nanjangud G.,

Chaganti R.S.K., Kuppers R., Dalla-Favera R.;

"Hypermutation of multiple proto-oncogenes in B-cell difficell lymphomas.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIINE=20130009; PubMed=10664448; DOI=10.1016/S0014-5793(00)01105-4; Koike N., Maita H., Taira T., Ariga H., Iguchi-Ariga S.M.M.; "Identification of heterochromatin protein 1 (HP1) as a phosphorylation target by Pim-1 kinase and the effect of phosphorylation on the transcriptional repression function of HP1."; FEBS Lett. 467:17-21(2000).
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"Identification of the human pim-1 gene product as a
cytoplasmic protein with tyrosine kinase activity.";
Mol. Cell. Biol. 8:1498-1503(1988).
                                                                                                                                                                                                                                                                                     This
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MEDLINE=22567470; PubMed=12680209;
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MEDLINE=88246418;
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                                                                                                                                                                                                                                                                                                                                                                   phosphoryiating HP1 gamma/CBX3.

CATALYTIC ACTIVITY: ATP + a protein = ADP + a SUBUNIT: Binds to RP9 (By similarity).

SUBCELULAR LOCATION: Cytoplasmic and nuclear. TISSUE SPECIFICITY: Expressed primarily in cell hematopoietic and germ line lineages.

PTM: Autophosphorylated on tyrosine residues.

SIMILARITY: Belongs to the Ser/Thr protein kin
                                                                                                                                                                                                                                              s Swiss-Prot entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the EM European Bioinformatics Institute. There are no restr
                                                                                                                                                                                                                                                                                                                                       subfamily.
DATABASE: 1
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WWW="http://www.infobiogen.fr/services/chromcancer/Genes/PIM1ID261.html"
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X-ray; X-ray; X-ray; X-ray;

mRNA. Genomic\_

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OST7177;
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O1-FEB-2005 (TrEMBLrel. 29, Created)
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O1-FEB-2005 (TrEMBLrel. 29, Last annotation update)
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PDB; 1Y14; X-ray; A=33-05.
PDB; 2BIK; X-ray; B=1-313.
PDB; 2BIL; X-ray; B=1-313.
Ensembl; ENSG00000137193; Homo s
HGNC; HGNC:8986; PIM1.
H-InvDB; HIX0005835; -.
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CONFLICT
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G0; G0:0005737; C:cytoplasm; TAS.
G0; G0:0004674; F:protein serine/threonine kinase activity;
G0; G0:0004678; F:protein serine/threonine kinase activity;
G0; G0:0007275; P:development; TAS.
G0; G0:0006468; P:protein amino acid phosphorylation; TAS.
InterPro; IPR008719; Forc kinase.
InterPro; IPR008271; Ser thr pkin_AS.
PF100069; Pkinase; I.
PF100069; Pkinase; I.
   Homo.
NCBI_TaxID=9606,
[1]
                                                                                                                   Homo sapiens (Human)
Eukaryota; Metazoa; (
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PROSITE; PS00107; PROTEIN KINASE DOM; 1
PROSITE; PS50011; PROTEIN KINASE ST; 1.
PROSITE; PS00108; PROTEIN KINASE ST; 1.
                                                                                          Mammalia;
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Serine/threonine-protein kinase; Transferase.
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                                                                                             Eutheria;
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35686
                                                                                          Euarchontoglires;
                                                                                                                Chordata;
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ATP (By similarity).
Proton acceptor (By s
ATP (By similarity).
AP -> RA (in Ref. 2).
AP -> RA (in Ref. 2).
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Pred. No. 5
                                                                                       Craniata; Vertebrata;
oglires; Primates; Cata
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                                                                                          Catarrhini;
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                                                                                                                      Euteleostomi;
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RESULT 7
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Best Local S
Matches 294
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R GO; GO:0005524; F:ATP binding; IEA.

R GO; GO:0004674; F:protein serine/threonine kinase activit
R GO; GO:0004671; F:protein-tyrosine kinase activit
R GO; GO:0004713; F:protein-tyrosine kinase activit
R GO; GO:0004713; F:protein-tyrosine kinase activit
R GO; GO:000468; P:protein amino acid phosphorylation; IEA.
R GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
R InterPro; IPR000271; Protein-tyrinase.
R InterPro; IPR002290; Ser_thr_pkinase.
R InterPro; IPR001245; Tyr_pkinase.
R INTERPO0069; Pkinase; I.
R SMART; SM00210; TyrKC; 1.
R SMART; SM00210; TyrKC; 1.
R SMART; SM00210; TyrKC; 1.
R PROSITE; PS0011; PROTEIN_KINASE_BT; 1.
R PROSITE; PS00101; PROTEIN_KINASE_BT; 1.
R PROSITE; PS00101; PROTEIN_KINASE_ST; 1.
R PROSITE; PS00101; PROTEIN_KINASE_Tyrinsferase.
SEQUENCE 313 AA; 35686 MW; 35BA76D3668E69A3 CRC64;
                                                                                                                                                                      Q9N0P9;
28-FEB-2003
28-FEB-2003
13-SEP-2005
NUCLEOTIDE SEQUENCE.
MEDLINE=21109090; PubMed=11182156;
Wang Z., Petersen K., Weaver M.S.,
                                                         Eukaryota; Metazoa; Chord
Mammalia; Eutheria; Laura
Pecora; Bovidae; Bovinae;
NCBI TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Laird G.;
Submitted (MAY-2005) to
-!- CATALYTIC ACTIVITY:
                                                                                                                           Bos taurus
                                                                                                                                           Name=PIM1;
                                                                                                                                                         Proto-oncogene
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SMR; QST7H7;
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CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
SIMILARITY: Belongs to the Ser/Thr protein kinase family.
L; AL353579; CAI20316.1; -; Genomic_DNA.
                                                                                                                                                                                                                                      BOVIN
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                                                                                                                           (Bovine).
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(Rel. 41,
(Rel. 48,
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                                                                                                                                                      el. 41, Last sequence update)
el. 48, Last annotation update)
serine/threonine-protein kinase
                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                               LSPGPSK
                                                                                              Chordata; Crani
Laurasiatheria;
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93.9%;
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Pred. No. 5.1e
LO; Mismatches
                                                                                              Craniata; Vertebrata;
heria; Cetartiodactyla;
    DOI=10.1016/S0165-2427(00)00259-2; Magnuson N.S.;
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les 9;
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                                                                                              Euteleostomi; Ruminantia;
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phosphoprotein

restrictions EMBL

9 18

a collaboration MBL outstation -

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RESULT 8
PIM3 COTJA

ID PIM3 COTJA STANDARD; PRT; 323 AA.

AC Q9PU85;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 13-SEP-2005 (Rel. 44, Last annotation update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Serine/threonine-protein kinase Pim-3 (EC 2.7.1.

GN Name=PIM3; Synonyms-PIM-3;
OS Coturnix coturnix japonica (Japanese quail).
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Best Local S
Matches 292
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ACT SITE
BINDING
SEQUENCE
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InterPro; IPR008271; Ser_thr_pkin_AS.
Pfam; PF00069; Pkinase; I.
ProDom; PD000001; Prot kinase; 1.
PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS00101; PROTEIN_KINASE_TOW; 1.
PROSITE; PS00101; PROTEIN_KINASE_TOW; 1.
PROSITE; PS00108; PROTEIN_KINASE_TOW; 1.
ATP-binding; Kinase; Nuclear protein; Nucleotide-binding; Phosphorylation; Proto-oncogene; Serine/threonine-protein
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ATP (By similarity).
Proton acceptor (By similarity).
ATP (By similarity).
; 9EF40229A847AD47 CRC64;
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Pred. No. 26
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Best Local S
Matches 208
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SEQUENCE
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ACT_SITE
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MEDLINE=20180111; PubMed=10713710; DOI=10.1038/sj.onc.1203355;

Eichmann A., Yuan L., Breant C., Alitalo K., Koskinen P.J.;

"Developmental expression of Pim kinases suggests functions also outside of the hematopoietic system.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ProDom; PD000001; Prot_kinase; 1.

SMART; SM00220; S.TKG; 1.

PROSITE; PS00107; PROTEIN KINASE ATP; 1.

PROSITE; PS50011; PROTEIN KINASE DOM; 1.

PROSITE; PS00108; PROTEIN KINASE ST; 1.

ATP-binding; Kinase; Nucleotide-binding; Phosphorylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Oncogene 19:1215-1224(2000).
-!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
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InterPro; IPR008271; Ser thr pkin AS.
InterPro; IPR002290; Ser thr pkinase.
Pfam; PF00069; Pkinase; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AJ130845; CAB62386.1; -; mRNA. HSSP; Q63450; 1A06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This Swiss-Prot entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the El the European Bioinformatics Institute. There are no resti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Archosauria;
Coturnix.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               removed.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                subfamily.
                                                                                                       300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                  MLLSKINSLAHLRARPCNDLHATKLAP--GKEKEPLESQYQVGPLLGSGGFGSVYSGIRV
                                                                                                                                                                                                    DIPFEHDEEIIKGQVFFRQTVSSECQHLIKWCLSLRPSDRPSFEEIRNHPWM-QGDLLPQ
                                                                                                                                                                                                                                                                                   RGEIKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCG
                                                                                                                                                                                                                                                                                                                                                             AASEIHLHSL
                                                                                                                                                                             DIPFEQDEEILRGRLYFRRRISPECQQLIKWCLSLRPSDRPTLEQIFDHQWMHKSEVVKS
                                                                                                                                                                                                                                                              TGELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSATVWSLGVLLYDMVCG
                                                                                                                                                                                                                                                                                                                                           VMERPELVKDLFDFITEKGALDEDTARGFFRQVLEAVRHCYGCGVVHRDIKDENLLVDLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MILSKFGSLAHICSPASMDHLPVKILPPVKVEKEPFDKVYQVGSVLGSGGFGTVYAGSRT
                                                                                                       EDCDIRLRTL
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46
168
69
323 /
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 as its content is in no way modified and this statement
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        STANDARD;
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168
69
36597 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                67.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 1131;
Pred. No. 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Protein kinase.
ATP (By similarity).
Proton acceptor (By similarity).
ATP (By similarity).
; E2A4FA20B6F6396C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
          326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; DB 1;
1.3e-75;
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Indels

4.

Gaps

119

178

297 239 238 60

28-FEB-2003 28-FEB-2003 13-SEP-2005

(Rel. (Rel.

41, Created)
41, Last sequence update)
48, Last annotation updat
protein kinase Pim-3 (EC 2

update) (EC 2.7.1.37)

Vertebrata; Euteleostomi; lires; Rodentia; Sciurognathi;

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S 밁 δ.

B

Name=Pim3

Serine/threonine-protein

Eukaryota; Metazoa; Mammalia; Eutheria; Mus musculus (Mouse)

Muroidea; Muridae; Murinae;

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                                                                                                     RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Stapleton M., Godin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Roberts S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Robak S.A., McTley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Wyers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Wyers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Wyers R.M.,
RA Rodriguez A.C., Schein J.E., Jones S.J.M., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length human Trand mouse cDNA sequences.";

Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

-- C. SIMILARITY: Belongs to the Ser/Thr protein kinase family. PIM
                                          Query Match
Best Local Sim
Matches 213;
                                                                                               Serine/threonine-protein ki

DOMAIN 40 293

NP BIND 46 54

ACT SITE 170 170

BINDING 69 69

SEQUENCE 326 AA; 35970 M
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                                                                                                                                                                                                                                                                                                                                                EMBL; BC017621; AAH17621.1; -; EMBL; BC026639; AAH26639; 1; -; HSSP; Q03656; 1HOW. Ensembl; ENSMUSG00000035828; M
                                                                                                                                                                                                                                                                                                                                                                                                                                         use as
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-FVB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUCLEOTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       European
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                subfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Swiss-Prot entry is copyright. It is produced een the Swiss Institute of Bioinformatics and European Bioinformatics Institute. There are r
                                                                                                                                                                                                                                                                                                                                                                                                                                        long
                                                         Similarity
MLLSKINSLAHLRARPC-----NDLHATKLAPGK-EKEPLESQYQVGPLLGSGGFGSVYS
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                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                         as its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DUENCE [LARGE SCALE MRNA].
TISSUE=Colon, and Salivary gland;
257; PubMed=12477932; DOI=10.1073/
L., Feingold E.A., Grouse L.H., De
                                                                                                                                                                                                                                                                                                                                                                                                                                      content is in no way
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Buarchontoglires; Glires;
Murinae; Mus.
                                                      67.4%;
71.0%;
                                                                                                   MΨ.
                                           31,
                                                                                               Protein kinase.
ATP (By similarity).
Proten acceptor (By s
ATP (By similarity).
ATP (By Fimilarity).
                                        Score 1123.5;
Pred. No. 4.8e
%1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                              mRNA.
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                                        5; DB 1;
.8e-75;
les 43;
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                                                                                                   CRC64;
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                                                                                                                                similarity)
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                                          Gaps
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activity;

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RESULT 10
                                                                        EMBL; AF086624; AAC68900.1

EMBL; AF057026; AAC36055.1

HSSP; QO3656; IHOW.

RGD; 620462; Pim3.

GG; GG:0004677; F:protein

GG; GG:0004677; P:autophos

GO; GG:0016572; P:histone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted [2]
GO; GO:0004674; F:protein serine/threonine kinase GO; GO:0046777; P:autophosphorylation; IDA. GO:0016572; P:histone phosphorylation; IDA. InterPro; IPR000719; Prot_kinase. InterPro; IPR008271; Ser_thr_pkinase. InterPro; IPR008271; Ser_thr_pkinase. Pfam; PF00069; Pkinase; I
                                                                                                                                                                                                                                         use
                                                                                                                                                                                                                                                                                              This
                                                                                                                                                                                                                                                                                                                                                                                                                     Feldman J.D., Vician L., Crispino M., Tocco G., Mar Bazan N.G., Baudry M., Herschman H.R.; Bazar N.G., Brotein kinase induced depolarization J. Biol. Chem. 273:16535-16543(1998).

-!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a protein = TISSUE SPECIFICITY: Present in a number of unst
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28-FEB-2003 (Rel. 41, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
Serine/threonine-protein kinase Pim-3 (EC 2.7.1.37)
Kid-1) (Kinase induced by depolarization).
Name=Pim3; Synonyms_Kid1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     070444;
28-FEB-2003
                                                                                                                                                                                                                        removed.
                                                                                                                                                                                                                                                                             between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=Sprague-Dawley;
Konietzko U., Kuhl D.;
"Pim-3 is a member of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28-FEB-2003 (Rel. 41,
28-FEB-2003 (Rel. 41,
13-SEP-2005 (Rel. 48,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Euarchonto
Muroidea; Muridae; Murinae; Ro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=98298176;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUCLEOTIDE SEQUENCE, AND CHARACTERIZATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rattus norvegicus (Rat).
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SIMILARITY: Belongs to t
                                                                                                                                                                                                                                                                                                                                                                                 including brain.
INDUCTION: By membrane depolarization
                                                                                                                                                                                                                                                          European
                                                                                                                                                                                                                                                                                                                                  subfamily.
                                                                                                                                                                                                                                                                                              Swiss-Prot
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  236
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GSRIADGLPVAVKHVVKERVTEWGSL-GGVAVPLEVVLLRKVGAAGGARGVIRLLDWFER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MLLSKFGSLAHL----CGPGGVDHLPVKILQPAKADKESFEKVYQVGAVLGSGGFGTVYA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (AUG-1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                         as
                                                                                                                                                                                                                                                      rot entry is copyright. It is produced through a collaboration Swiss Institute of Bioinformatics and the EMBL outstation - Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3176; PubMed=9632723; DOI=10.1074/jbc.273.26.16535;
Vician L., Crispino M., Tocco G., Marcheselli V.L
audry M., Herschman H.R.;
                                                                                                                                                                                                                                         its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                         content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chordata; Craniata; Vertebrata; Euteleostomi;
Euarchontoglires; Glires; Rodentia; Sciurogna
Murinae; Rattus.
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Q4VSULT
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                           Richards F. L., Peingold E.A., Grouse L.H., Derge J.G.,
A Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
A hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
A Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
A Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
A Stapleton M., Gudlin T.B., Toshiyuki S., Carninci P., Prange C.,
A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
A Hitchards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A Hitchards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
A Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
A Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
A Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
A Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local S
Matches 213
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M2 RAT
Q4V8M2 RAT
Q4V8M2;
13-SEP-2005
13-SEP-2005
13-SEP-2005
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PROSITE; PS001107; PROTEIN KINASE DOM; 1.

PROSITE; PS50011; PROTEIN KINASE DOM; 1.

PROSITE; PS50011; PROTEIN_KINASE_ST; 1.

ATP-binding; Kinase; Nuclectide-binding; Phosphorylation; Serine/threonine-protein kinase; Transferase.

DOMAIN

40
293
Protein kinase; Transferase.

DOMAIN

45
479 (By similarity).

BINDING

69
69
ATP (By similarity).
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MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;
MEDLINE=2238257; Pelngold E.A., Grouse L.H., Derge J.G.,
Strausberg R.L., Feingold E.A., Grouse L.H., Schuler
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurogna
Muroidea; Muridae; Murinae; Rattus.
MCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13-SEP-2005 (TrEMBLrel. 31, Created)
13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation updat
13-SEP-2005 (TrEMBLrel. 31, Last annotation updat
Hypothetical protein (Fragment).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GIRVADNLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKV--SSDFSGVIRLLDWFER
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   CDNA
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71.0%;
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Pred. No. 5.7e-75;
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ATP (By similarity).
Proton acceptor (By similarity)
ATP (By similarity).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Glires; Rodentia; Sciurognathi;
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Best Local S
Matches 213
                                                                                                                                                                                                  PIM3_HUMAN STANDARD; PRT; 326 AP
Q86V86; Q68BM2;
29-MAR-2004 (Rel. 43, Created)
29-MAR-2004 (Rel. 43, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
Serine/threonine-protein kinase Pim-3 (EC 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ProDom; pD000001; Prot_kinase; 1.

SMART; SM00220; TyrKc; 1.

SMART; SM00219; TyrKc; 1.

SMART; SM00219; TyrKc; 1.

PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.

PROSITE; PS00101; PROTEIN_KINASE_DOM; 1.

PROSITE; PS00108; PROTEIN_KINASE_DOM; 1.

ATP-binding; Hypothetical_protein; Kinase; Nucleotide-binding;
                                                      TISSUE=Liver;
PubMed=15540201; DOI=10.1002/ijc.20719;
PubMed=1540201; DOI=10.1002/ijc.20719;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Serine/threonine-protein kinase; Transferase.
NON_TER 1 1 1
SEQUENCE 380 AA; 41568 MW; F82BE8E50DD713
          Fujii C., Nakamoto Y., Lu P., Tsuneyama K., Popivanova Kaneko S., Mukaida N., "Aberrant expression of serine/threonine kinase Pim-3 hepatocellular carcinoma development and its role in to of human hepatoma cell lines.";
                                                                                                                                                                                                                                                                                HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted
                                                                                                                                      Homo.
                                                                                                                                                    Mammalia;
                                                                                                                                                                           Homo sapiens (Human)
                                                                                                                                                                                          Name=PIM3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00069; Pkinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NIH MGC Project;
                                                                                               NUCLEOTIDE SEQUENCE [MRNA], FUNCTION,
                                                                                                                         NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro;
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213; Conserv
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                                                                                                                                                                                                                                                                                                                                              YDMVCGDIPFEHDEEIIKGQVFFRQTVSSECQHLIKWCLSLRPSDRPSFEEIRNHPWMQG
                                                                                                                                                                                                                                                                                                                                                                                                                                PDGFLLVLERPEPAQDLFDFITERGALDEPLARRFFAQVLAAVRHCHNCGVVHRDIKDEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                 PDSFVLILERPEPVQDLFDFITERGALQEDLARGFFWQVLEAVRHCHNCGVLHRDIKDEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GIRVADNLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKV--SSDFSGVIRLLDWFER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MILISKINSLAHLRARPC----NDLHATKLAPGK-EKEPLESQYQVGPLLGSGGFGSVYS 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GSRIADGLPVAVKHVVKERVTEWGSL-GGMAVPLEVVLLRKVGAAGGARGVIRLLDWFER
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IPR008271; Ser thr pkin AS.
IPR002290; Ser thr pkinase.
IPR001245; Tyr pkinase.
                                                                                                                                                  ; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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Pred. No. 6.9e.
31; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99:16899-16903 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        F82BE8E50DD71346 CRC64;
                                                                                                   AND
                                                                                                                                                                                                    update)
(EC 2.7.1.37).
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                                                            Popivanova B
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RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altechul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altechul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Warusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Warusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Raha S.S., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Altering M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Rahey J., Halton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Rahesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Shein J.E., Jones S.J.M., Marra M.A.,
"Generation and initial analysis of more than 15,000 full-length human and many septences".
                                                                                                                                                  Query Match
Best Local S
Matches 216
                                                                                                                                                                                                                                                                                              Serine/threonine-protein k
DOMAIN 40 293
NP BIND 46 54
ACT SITE 170 170
BINDING 69 69
                                                                                                                                                                                                                                                                   NP_BIND
ACT_SITE
BINDING
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00069; Pkinase; 1.

Prodom; PD000001; Prot kinase; 1.

PROSITE; PS00107; PROTEIN KINASE ATP; 1.

PROSITE; PS50011; PROTEIN KINASE DOM; 1.

PROSITE; PS00108; PROTEIN KINASE ST; 1.

ATP-binding; Kinase; Nucleotide-binding; Phosphorylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IDENTIFICATION FROM ESTS.

MEDLINE=22682943; PubMed=12798037; DOI=10.1016/S1476-9271(02)00095-6; Chichester C., Nikitin F., Ravarini J.-C., Lisacek F.; "Consistency checks for characterizing protein forms."; "Consistency checks for characterizing protein forms."; Comput. Biol. Chem. 27:29-35(2003).

-!- FUNCTION: May be involved in cell cycle progression and antiapoptosis process. Implicated in proliferation of human hepatoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR000719; Prot kinase.
InterPro; IPR008271; Ser_thr_pkin_AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AB114795; BAD42438.1; -;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUCLEOTIDE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cell lines.

CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.

TISSUE SPECIFICITY: Widely expressed. No expression in colon,
thymus, and small intestine. Expressed in human hepatoma cell
lines but not in normal liver tissues.

SIMILARITY: Belongs to the Ser/Thr protein kinase family. PIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mouse cDNA sequences.";
c. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         as long as its content is in no way modified
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Swiss-Prot entry is copyright. It is produced through sen the Swiss Institute of Bioinformatics and the EN European Bioinformatics Institute. There are no resti
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bl; ENSG00000198355;
                                                                                                                                                                                Similarity
                                                                   MLLSKINSLAHLRARPC-----NDLHATKLAPGK-EKEPLESQYQVGPLLGSGGFGSVYS
                                    MLLSKFGSLAHL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
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                                                                                                                                                  Conservative
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                                                                                                                                                                             67.1%;
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                                    -CGPGGVDHLPVKILQPAKADKESFEKAYQVGAVLGSGGFGTVYA
                                                                                                                                                                                                                                                                                                                                                                                                               kinase; Transferase.
                                                                                                                                                                                                                                                                      MW;
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                                                                                                                                            Score 1119; D
Pred. No. 1e-7
35; Mismatches
                                                                                                                                                                                                                                                                                              ATP (By similarity).
Proton acceptor (By
ATP (By similarity).
                                                                                                                                                                                                                                                                      41FDF9DD2467A162
                                                                                                                                                                             1119; DB 1;
No. 1e-74;
                                                                                                                                                                                                                                                                      CRC64;
                                                                                                                                                                                                                                                                                                                               similarity).
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PIM3 XENLA

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69
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                                                                                        291
54
168
69
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REMBL; L29495; AAA8550.

R InterPro; IPR000719; Prot kinac.

R InterPro; IPR000871; Ser_thr_pkin_AS.

Pfam; PF00069; Pkinase; 1.

DR Pfam; PF00069; Pkinase; 1.

PROSITE; PS00107; PROTEIN KINASE ATP; FALSE_NEG.

PROSITE; PS0011; PROTEIN KINASE_DOM; 1.

PROSITE; PS000108; PROTEIN KINASE_ST; 1.

PROSITE; PS00108; PROTEIN KINA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-DEC-1998 (Rel. 37, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update
Serine/threonine-protein kinase Pim-3 (EC 2
Name=PIM3; Synonyms=PIM1;
Kenopus laevis (African clawed frog).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This Swiss-Prot entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use as long as its content is in no way modified and this statuse as long as its content is in no way modified and this statuse as long as its content is in no way modified and this status as long as its content is in no way modified and this status as long as its content is in no way modified and this status as long as its content is in no way modified and this status as long as its content is in no way modified and this status as long as its content is in no way modified and this status as long as its content is in no way modified and this status as long as its content is in no way modified and this status as long as its content is in no way modified and this status as long as its content is in no way modified and this status as long as its content is in no way modified and this status as long as its content is in no way modified and this status as long as its content is in no way modified and this status as long as its content is in no way modified and this status as long as its content is in no way modified and this status as long as lon
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MEDLINE=97256766; PubMed=9099695; DOI=10.1074/jbc.272.16.10514;
Palaty C.K., Kalmar G., Tai G., Oh S., Amankawa L., Affolter M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Ven
Amphibia; Batrachia; Anura; Mesobatrachia;
Xenopodinae; Xenopus; Xenopus.
MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Palaty C.K., Kalmar G., Tai G., Aebersold R., Pelech S.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Identification of the autophosphorylation sites im-1 proto-oncogene-encoded protein kinase.";
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SIMILARITY: Belongs to the Ser/Thr protein kinase family.
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CATALYTIC ACTIVITY: ATP + a protein = ADP + a
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Proton acceptor (By similarity).
ATP (By similarity).
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(EC 2.7.1.37) (Pim-1)
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RESULT 14
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ID Q811X8 MOUSE P
AC Q811X8;
DT 01-UNU-2003 (T
DT 01-MAR-2004 (T
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                                                                                                            Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.

1. SIMILARITY: Belongs to the Ser/Thr protein kinase family.

2. PEMBL; AY026239; AAK16606.1; -; mRNA.

2. MSSP; Q03656; 1Q99.

2. MR; Q01565; 1Q99.

2. MR; Q011X8; 36-292.

3. MGI; MGI:1352297; Pim3.

3. MGI; MGI:1352297; Pim3.

3. MGI; MGI:1352297; Pim3.

3. GO; GO:0000524; F:ATP binding; IEA.

3. GO; GO:0006468; P:protein serine/threonine kinase activity; IEA.

3. GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.

3. GO; GO:0004674; P:protein mino acid phosphorylation; IEA.

3. Interpro; IPR000719; Prot kinase.

3. Interpro; IPR008271; Ser_thr_pkin_AS.

3. Ffam; PP00069; Pkinase; 1.

3. Probom; PD0000017; PROTEIN_KINASE_ATP; 1.

3. PROSITE; PS00107; PROTEIN_KINASE_TOM; 1.

3. PROSITE; PS00108; PROTEIN_KINASE_ST; 1.

3. PROSITE; PS00108; PROTEIN_KINASE_TOM; 1.

4. PROSITE; PS00108; PROTEIN_KINASE_TOM; 1.

4. PROSITE; PS00108; PROTEIN_KINASE_TOM; 1.

5. PROTEIN_KINASE_TOM; 1.

5. PROTEIN_KINASE_TOM; 1.

5. PROTEIN_KINASE_TOM; 1.
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Best Local S
Matches 208
Query Match
Best Local Similarity
Matches 212; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Name=Pim3; Synonyms=Kid1; Mus musculus (Mouse).
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   Conservative
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Last sequence up
Score 1110; DB 2;
Pred. No. 4.8e-74;
2; Mismatches 42
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Pred. No. 2
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AB4DD61E7A99A38F CRC64;
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RESULT 15
Q66111 XENTR
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D1 25-OCT-2004 (TREMBLrel. 28,
DT 25-OCT-2004 (Western
OC Amphibia, Batrachia, Anura;
OC Amphibia, Batrachia, Anura;
OC Amphibia, Batrachia, Feingold E
RN NCLEOTIDE SEQUENCE.
TISSUB=Embryo;
RN (1)
RN Altschul S.F., Zeeberg B.B.,
RN RABA S.S., Loquellano N.A.,
RN Stapleton M.J., Usdin T.B.,
RN Altschul S.F., Zeeberg B.B.,
RN RABA S.S., Loquellano N.A.,
RN Altschul S.F., Zeeberg B.B.,
RN RABA S.S., Loquellano N.A.,
RN Altschul S.F., Zeeberg B.B.,
RN RABA S.S., Loquellano N.A.,
RN Altschul S.F., Zeeberg B.B.,
RN RABA S.S., Loquellano N.A.,
RN Altschul S.F., Zeeberg B.B.,
RN RABA S.S., Loquellano N.A.,
RN Bosak S.A., McEwan P.J.,
NN CEBART D.J.,
NN CEBART D.J.,
RN CEBART D.
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                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE-Embryo;

Riein S., Gerhard D.S.;

Riein S., Gerhard D.S.;

Submitted (AUG-2004) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
-!- SIMILARITY: Belongs to the Sey/Thr protein kinase family.

EMBL, BC081340; AAH81340.1; -; mRNA.

EMBL, BC081340; AAH81340.1; -; mRNA.

SMR, Q66III; 32-297.

Ensembl, ENSXETG0000009354; Xenopus tropicalis.
G0; G0:0005524; F:ATP binding; IEA.
G0; G0:0004674; F:protein serine/threonine kinase activity; IEA.
G0; G0:0004713; F:protein-tyrosine kinase activity; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Xenopus tropicalis (Western clawed frog) (Silurana tropicalis).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                            "Generation and initial analysis and mouse cDNA sequences.";
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annotation update)
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Best Local Simi
Matches 198;
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JR InterPro; IPR008271; Ser_thr_pkin_AS.

JR InterPro; IPR008271; Ser_thr_pkinase.

JR InterPro; IPR001290; Ser_thr_pkinase.

JR InterPro; IPR001245; Tyr_pkinase.

JR InterPro; IPR001245; Tyr_pkinase.

JR Pfam; PF00069; Pkinase; 1.

JR ProDom; PD000001; Prot_kinase; 1.

JR ProDom; PD000001; Prot_kinase; 1.

JR SWART; SM00220; S_TKC; 1.

JR SWART; SM00220; S_TKC; 1.

JR SWART; SM00219; TYKC; 1.

JR SWART; SM00219; TYKC; 1.

JR PROSITE; PS00107; PROTEIN KINASE_DOM; 1.

JR PROSITE; PS00101; PROTEIN KINASE_DOM; 1.

JR PROSITE; PS00101; PROTEIN KINASE_ST; 1.

JR PROSITE; PS00101; PROTEIN KINASE_ST; 1.

JR PROSITE; PS00101; PROTEIN KINASE_ST; 1.

KW ATP-binding; Cell cycle; Cell division; Kinase; Nucleotide-binding;

KW Serine/threonine-protein kinase; Transferase.

SQ SEQUENCE 318 AA; 36547 MW; 48CCF12797F01FDC CRC64;
                                                                                                                     177
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                                                                                                                                                                                                                                                                                                                   h 65.2%; Score 1087; DB 2; Similarity 67.1%; Pred. No. 2.4e-72; 98; Conservative 42; Mismatches 47;
                                                                                                                  DIPFEHDEEIIKGQVFFRQTVSSECQHLIKWCLSLRPSDRPSFEEIRNHPWMQGD 293
                                                                                                                                                                              ILERPEPVQDLFDFITERGALQEDLARGFFWQVLEAVRHCHNCGVLHRDIKDENILIDLS 178
                                                                                                                                                                                                                                      MSSVQVIYH---QKIHNYHLNSVFPKDDLPAVKEPFENCYQVGPVIGTGGFGTVYSGVRI
               2006, 05:18:58
                                                                                                                                                                                                                                                                                                                                                                                          Length 318;
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